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01.900

Bowman,



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OM nucleic - nucleic search, using sw model

Run on:

August 6, 2005, 09:58:01; Search time 1445 Seconds (without alignments) 670.660 Million cell updates/sec

US-10-773-678-342 20 1 gactcttgcaggaagcggct 20 Title: Perfect score:

IDENTITY NUC Gapox 1.0 Scoring table: Sequence:

4708233 segs, 24227607955 residues Searched:

790860 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

3b pr: *
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3b wi: * gb_ba:* gb_htg:* gb_in:* gb_ogt gb_oat: gb_pat: gb_pl:** GenEmbl:* 6: 7: 8: 9: 10: 11: 13: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	% Query Match	* Query Match Length DB	. 80	ID	Description
	14	70.0	20	9	AR120998	AR120998 Sequence
7	14	70.0	20	9	BD272619	BD272619 Antisense
m	14	70.0	20	9	AR531367	AR531367 Sequence
4	13	65.0	19	4	DOGP45501	L24340 Dog (Clone:
ı.	12.8	64.0	20	9	BD228539	BD228539 IL-17 hom
9	12.8	64.0	20	9	AR359764	AR359764 Sequence
2	12.6	63.0	20	9	CO798932	CQ798932 Sequence
	12.4	62.0	17	9	A89364	A89364 Sequence 15
o	12.4	62.0	17	9	AX672730	AX672730 Sequence
10	12.4	62.0	17	9	AX762313	AX762313 Sequence
11	12.4	62.0	17	9	BD066877	BD066877 An antise
12	12.4	62.0	18	9	AX117443	AX117443 Sequence
c 13	12.4	62.0	20	9	AR098941	AR098941 Sequence
14	12.4	62.0	20	9	AR164768	AR164768 Sequence
15	12.4	62.0	20	ď	BD222879	BD222879 KVLQT1-QT
0 16	12.4	62.0	20	9	179781	179781 Sequence 77
c 17	12.4	62.0	20	9	AR218732	AR218732 Sequence
c 18	12.4	62.0	20	9	AR223147	AR223147 Sequence
c 19	12.4	62.0	20	9	AR229909	AR229909 Sequence

S Sequence S Sequence A Sequence 7 Sequence 2 Sequence 5 Sequence 5 Sequence 5 Sequence 5 Sequence 6 Regulat 6 Regulat	AX21555 Sequence AX64838 Sequence AX64838 Sequence AX64838 Sequence AX64838 Sequence AX16615 Sequence AX16615 Sequence AX16615 Sequence AX361459 Sequence AX361459 Sequence AX361545 Sequence AX361545 Sequence AX062314 Sequence AX062315 Sequence CX0612375 Sequence CX0612375 Sequence CX0612375 Sequence CX0612375 Sequence CX0612376 Sequence CX0612377 Sequence CX0612377 Sequence CX0612477 Sequence CX0612475 Sequence CX0612475 Sequence CX0612475 Sequence CX0621475 Sequence CX0621475 Sequence CX0621476 Sequence CX0621476 Sequence CX0621476 Sequence CX0621476 Sequence CX0621476 Sequence AX456441 Sequence AX456441 Sequence AX456441 Sequence AX46233 Sequence AX462341 Sequence AX61314 Sequence AX462341 Sequence AX462341 Sequence AX462341 Sequence AX61314 Sequence	Sequents Seq
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12.2.4 62. 12.2.2 611. 12.2.2 611. 12.2.2 611. 12.2.2 611. 12.2 611. 13.8 60. 11.8 59.		11.4 11.1 11.1 11.1 11.1 11.1 11.2 11.2

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1 (bases 1 to 19)

Ostrander, B.A., Mapa, F.A., Yee, M. and Rine, J.
One hundred and one new simple sequence repeat-based markers for the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Original source text: Canis familiaris (library: E. Ostrander, in pBluescript+) adult spleen DNA.
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Fred Hutchinson Cancer Research Center

Transplantation Bology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
Seattle, WA 98104, USA
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
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                                                                            Query Match 70.0%; Score 14; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 9.7e+04; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    linear
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124340
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100.0%; Pred. No. 9.7e+04;
rative 0; Mismatches 0;
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PCR identification; PCR primer; STS.
1 of 2 canis familiaris (dog)
Canis familiaris
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/organism="unknown"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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Karras, J.G.
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AR464436 Sequence
AR464438 Sequence
AX728547 Sequence
AX760524 Sequence
BD244848 Polymucle
BD244849 Polymucle
AX023724 Sequence
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                                                                                                                                          AX023725 Sequence
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Autisense oligonucleotide modulation of STAT3 expression
Patent: JP 2002541784-A 19 10-DEC-2002;
ISIS PHARMACEUTICALS INC
ISIS PHARMACEUTICALS INC
ON Artificial Sequence
PN JP 2002541784-A/19
PD 10-DEC-2002
PF 06-APR-1999 US 09/288461
PR 08-APR-1999 US 09/288461
PI JAMES G RARRAS
PC C12N15/09, A61R31/711, A61R48/00, A61P29/00, A61P29/00, A61P3/09, C12N15/09, C12N15/00, C12N15/00, C12N15/09, A61P3/09, C12N15/09, A61P3/09, A61P3/0
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Unclassified.
1 (bases 1 to 20)
3 Karras,J.G.
Antisense modulation of stat3 expression
AL Patent: US 6159694-A 19 12-DEC-2000;
Location/Qualifiers
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/organism="synthetic construct"
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                  AR464438
AX728547
AX760524
BD244848
BD244849
AX023724
                                                                                                                                          AX023725
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JP 2002541784-A/19.
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      7 GACTCTTGCAGGAA 20
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synthetic construct
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PAT 22-JAN-2000
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    .20
    /organism="synthetic construct"
    /mol Lype="unassigned DNA"
    /db xref="taxon:32630"
    /noce="Artificially synthesized primer sequence for RT-PCR"

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Method for diagnosing pancreatic cancer
Patent: WO 2004031412-A 13 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
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                  linear
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Gatanaga,T. and Granger,G.A.
Tumor necrosis factor receptor releasing enzyme
Patent: US 6593456-A 134 15-JUL-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          64.0%; Score 12.8; DB 6;
87.5%; Pred. No. 3.7e+05;
tive 0; Mismatches 2;
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CQ798932
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Sequence 1512 from Patent WO9833904.
A89364
           20 bp Di
Sequence 134 from patent US 6593456.
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/organism="unknown"
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1 (bases 1 to 17)
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1 (bases 1 to 20)
Chen, J., Filvarofff, E., Goddard, A., Gurney, A.L., Li, H. and Wood, W.I.
IL-17 homologous polypeptide and its application to remedy
Batent: JP 2002515246-A 134 28-MAY-2002;
GENENTECH INC
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Strandedness: Single;

Topology: Linear;

Topology: Linear;

IL-17 homologous polypeptide and its application to remedy FH

Location/Qualifiers
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PN JP 2002515246-A/134
PD 20-WAY-2002
PP 14-MAY-1999 JP 2000549734
PR 15-MAY-1999 US 60/085579, 23-DEC-1998 US 60/113621 PI
JIAN CHEN, ELLEN FILVAROFF, AUDLEY GODDARD, AUSTIN L GURNEY, PI
HANZHONG LI,
PI WILLIAM I WOOD
PC C12N15/09, A61K38/21, A61K45/00, A61P19/00, C07K14/52, C07K16/24,
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/organism="Canis familiaris"
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/tissue_lib="E. Ostrander, in pBluescript+"
1..19
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                                                                                                                                                                                                                                 ch 65.0%; Score 13; DB 4; Length 19; l Similarity 100.0%; Pred. No. 3e+05; 13; Conservative 0; Mismatches 0; Indels
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
Location/Qualifiers
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JP 2002515246-A/134.
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1 TCTTCCAGGAAGCTGC 16
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PC C07K19/00,
PC C12N1/19, C12Q1/68, C12N15/00,
PC A61K37/66, C12N5/00,
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5 BD228539

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REFERENCE AUTHORS TITLE JOURNAL

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FEATURES

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PAT 27-AUG-2002
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Schlingensiepen, K.H. and Brysch, W.
An antisense Oligonucleotide preparation method
Patent: JP 2001511000-A 1512 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP. 2001511000-A/1512
JO-JAN-1998 JP 1998532533
31-JAN-1997 EP 97101531.8
KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
C12N15/11, C07H21/04, A61K31/70
An antisense oligonucleotide preparation method FH
Location/Qualifiers
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                                                                                                    6; Length 17;
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An antisense oligonucleotide preparation method.
BD066877
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Location/Qualifiers
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Best Local Similarity 92.9%; Pred. No. 6e+05;
Matches 13; Conservative 0; Mismatches
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Sequence 2566 from Patent WO0129262.
AX117443

    .17
/organism="Homo sapiens"
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AX117443
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
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Brysch, W. and Schlingensiepen, K.
AN ANTISENSE OLICONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 1512 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1175 from Patent W003004526. AX672730
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 5634 from Patent WO03040369.

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AX762313
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

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E 20 20)
E 20 20)
E 3 (bases 1 to 20)
E 4 (bases 1 to 20)
E 6 (bases 1 to 20)
E 7 (bases 1 to 20)
E 8 (baring, M.T., Sanguinetti, M.C., Karan, M.E., Landes, G.M.,
COMDOTS, T.D., Burn, T.C. and Splawski, I.

EVULT-OT extension syndrome
L 8 Patent: JP 2003521045-A 77 16-UUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION, GENZYME CORP
OS Homo sapiens (human)
EN JP 2002521045-A 777
ED 16-UUL-2002
EP 12-MAY-1999 UP 200562052
EP 29-UUL-1999 US 60/094477, 17-AUG-1998 US 09/135010 FI
MARK T KEATING, MICHAEL C SANGUINETTI, MARK E KARAN, GREGORY M PI
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                                                            PAT 17-JUL-2003
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C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12N1/21, C12N5/10, C12P21/08, C12Q1/02, C12Q1/68, G01N33/15, G01N33/ PC
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CLZN15/09, A01K67/027, C07K14/46, C07K14/47, C07K16/18, C1ZN1/15, PC
C1ZN1/19,
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Trofatter, J.A., MacCollin, M.M. and Gusella, J.F.
Tumor suppressor gene merlin
Patent: US 5707863-A 77 13-JAN-1998;
Location/Qualifiers
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Key Location/Qualifiers
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Sequence 77 from patent US 5707863.
179781
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/organism="Homo sapiens"
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KVLQTI-QT extension syndrome.
BD222879
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                                                                                                               BD222879.1 GI:33032649
JP 2002521045-A/77.
Homo sapiens (human)
Homo sapiens
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Keating, M.T., Sanguinetti, M.C. and Splawski, I.
Mutations in the KCNE1 gene encoding human minK which cause
arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
Patent: US 6274332-A 79 14-AUG-2001;
Location/Qualifiers
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Trofatter, J.A., MacCollin, M.M. and Gusella, J.F.
Tumor suppressor merlin and antibodies thereof
Patent: US 6077685-A 77 20-JUN-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.0%; Score 12.4; DB 6; 92.9%; Pred. No. 5.9e+05; iive 0; Mismatches 1;
         /organism="synthetic construct"
/mol.type="unassigned DNA"
/mol.type="taxon:32630"
/note="primer"
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Sequence 79 from patent US 6274332.
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/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 77 from patent US 6077685.
AR098941.1 GI:12808707
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AR164768.1 GI:16237937
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Tobases I to 20)

Keating, M.T., Sanguinetti, M.C. and Splawski, I.

Mutations in the KCNEI gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6323026-A 79 27-NOV-2001;
Location/Qualifiers
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    PAT 20-DEC-2002
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1 (Dases 1 to 20)

Reating, M.T., Sanguinetti, M.C., Curran, M.E., Landes, G.M., Connors, T.D., Burn, T.C. and Splawski, I.

Diagnostic method for KVLQT1.-a long QT syndrome gene Patent: US 6582913-A 79 24-JUN-2003;
                                                                                                               Unclassified.

(bases 1 to 20)

Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.

KVLQTI-a long QT syndrome gene
Patent: US 6451534-A 79 17-SEP-2002;
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Sequence 79 from patent US 6582913.
AR344603
20 bp I Sequence 79 from patent US 6451534. AR229909
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Sequence 79 from patent US 6323026.
AR262165
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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AR344603/c
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1 (bases 1 to 20)

Keating,M.T., Sanguinetti,M.C. and Splawski,I.

Mutations in the KCNEI gene encoding human mink which cause
arrhythmia susceptibility thereby establishing KCNEI as an LQT gene
Patent: US 6432644-A 79 13-AUG-2002;
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Keating, M.T., Sanguinetti, M.C., Curran, M.B., Landes, G.M., Connors, T.D., Burn, T.C. and Splawski, I.
KVLQT1--a long qt syndrome gene Patent: US 6420124-A 79 16-JUL-2002;
Location/Qualifiers
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                                     62.0%; Score 12.4; DB 6; Length 20; 92.9%; Pred. No. 5.9e+05; ive 0; Mismatches 1; Indels
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92.9%; Pred. No. 5.9e+05;
tive 0; Mismatches 1;
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/mol_type="genomic DNA"
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AR218732.1 GI:23319627
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Matches 13; Conservative
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AR223147/c LOCUS DEFINITION

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synthetic construct
other sequences; artificial sequences.
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Sequence 1380 from Patent WO0130362.
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Sequence 166 from Patent WO0063441.
AX039777
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Location/Qualifiers
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AX130162.1 GI:14136467
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          TCTTGCAGGAAGCGGCT 20
                        17 ATTCTTGCACGAACGG 1
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
                                                                                                                                                                                                                                                                                                                                                                                               Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
Myosin-like gene expressed in human heart and muscle
Patent: WO 0192224-A 8114 06-DEC-2001;
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                                                                                 Query Match 62.0%; Score 12.4; DB 6; Length 20; Best Local Similarity 92.9%; Pred. No. 5.9e+05; Matches 13; Conservative 0; Mismatches 1; Indels
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Sequence 8114 from Patent WO0192524.
CQ623374.1 GI:41673592
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="PCR primer"
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Regulation of repressor genes using nucleic acid molecules.
BD259354
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A61K37/02,
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PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN C12N15/09, AGIK38/00,A61P43/00,A61P43/00,C12NS/10, PC 12P21/02,
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Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
Pegulation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 7147 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
                                                                                    (Dases 1 to 20)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Blailellic markers for use in constructing a high density disequilibrium map of the human genome
Patent: US 6537751-A 8500 25-MAR-2003;
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                                                                                                                                                                                                                                                                              60.0%; Score 12; DB 6; Length 20; 75.0%; Pred. No. 9.2e+05; ive 0; Mismatches 5; Indels
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 GI:31684049
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             17 bp DNA
Sequence 3140 from Patent W003004526.
AX674695
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Patent: WO 03025175-A 397 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 8500 from patent US 6537751.
AR296765
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Sequence 397 from Patent WO03025175.
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                                                                                       AX674695.1 GI:29333043
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Homo sapiens
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Best Local Similarity
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AR296765/c
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AUTHORS
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RESULT 26
AX674695
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PAT 07-SEP-2001
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                                                          AGIK37/02, (CI2N1:91)
(CI2N5/00,C12R1:91)
Regulation of repressor genes using nucleic acid molecules FH Location/Qualifiers
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                                           (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
Patent: WO 0159103-A 91 16-AUG-2001;
RIBOZYME HARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
Location/Qualifiers
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,
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Location/Qualifiers
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86.7%; Pred. No. 1.2e+06;
tive 0; Mismatches 2;
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Pred. No. 1.2e+06;
0; Mismatches 2;
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/mol_type="unassigned RNA"
/db_xref="taxon:3260"
/nofe="Nucleic Acid"
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Sequence 92 from Patent WO0159103.
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Sequence 91 from Patent WO0159103.
AX214649
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/organism="unidentified"
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PN JP 2002541795-A/7148
PD 10-DEC-2002
PP 11-APR-12000 JP 2000611654
PP 12-APR-1999 US 60/123390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC PC
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PN JP 2002541795-A/7149
PN JP 2002541795-A/7149
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PR 12-APR-1999 US 60/129390
C12N15/09, A61K38/00, A61K48/00, A61P43/00, C12N5/10, PC C12P21/02,
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BD259356
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1 (bases 1 to 17)

Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.

squlation of represer genes using nucleic acid molecules Patent: JP 2002541795-A 7149 10-DEC-2002;

RIBOZYME PHARMACEUTICALS INC
                                    HDZ59155 17 bp DNA linear PAT 17·
Regulation of repressor genes using nucleic acid molecules.
BDZ59155
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Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Sagnlation of repressor genes using nucleic acid molecules Patent: JP 2002541795-A 7148 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
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Location/Qualifiers
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86.7%; Pred. No. 1.2e+06;
iive 0; Mismatches 2;

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(C12N5/00,C12R1:91)
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JP 2002541795-A/7149.
                                                                                                BD259355.1 GI:33069125
JP 2002541795-A/7148.
unidentified
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Best Local Similarity
Matches 13; Conserv
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PC (C12P)
PC A61K3:
PC (C12N)
CC Regul
Key FT SOUTC
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ACCESSION
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TITLE
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AUTHORS
                  RESULT 30
BD259355
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JOURNAL
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PAT 22-MAR-2003
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                  Score 11.8; DB 6; Length 17;
Pred. No. 1.2e+06;
0; Mismatches 2; Indels
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Patent: EP 1273660-A 226 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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Patent: EP 1277566-A 227 08-JAN-2003;
Aeomica, Inc. (US)
Location/Qualifiers
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ΑΧ648387
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Sequence 226 from Patent BP1273660.
AX648386

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                                                                                   Query Match 59.0%;
Best Local Similarity 86.7%;
Matches 13; Conservative 0
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Homo sapiens
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Homo sapiens
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16 TCATGCAAGAAGCGG 2
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AX648386/c
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AX648387/c
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0159103-A 92 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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Human sodium-hydrogen exchanger like protein 1
Patent: EP 1273660-A 225 08-JAN-2003;
Aeomica, Inc. (US)
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Sequence 997 from Patent WO0159103.
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Sequence 1738 from Patent WO0129262.
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Sequence 130 from patent US 6258600.
AR162450
AR162450.1 GI:16229633
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AR067594.1 GI:5998816
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AUTHORS Gray, J. W. and Waier, H.-U.G.

TITLE Quantitative DNA fiber mapping
JOURNAL Patent: US S851769-A 1 22-DEC-1998;

Location/Qualifiers

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ORIGIN

Query Match

S8.0%; Score 11.6; DB 6; Length 20;

Best Local Similarity 77.8%; Pred. No. 1.4e+06;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps

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Qy I. CARTCTTGCAGGAAGCGG 3

Search completed: August 6, 2005, 16:01:15

Job time: 1449 secs
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Sequence 19, Application US/09758881

Sequence 19, Application US/09758881

Sequence 19, Application US/09758881

GENERAL INFORMATION:

APPLICANT: Karras, James G

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

FILE REPRENCE: ISPH-0532

CURRENT APPLICATION NUMBER: US/09/758,881

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 152

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 20
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Sequence 19, Application US/09288461

SERNERAL INFORMATION:

APPLICANT: Karras, James G.

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT FILING DATE: 1999-04-08

CURRENT FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 19
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.0%; Score 14; Best Local Similarity 100.0%; Pred. No. Matches 14; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Synthetic Sequence
US-09-288-461-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Matches 14; Conservative
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                                                                                  US-09-288-461-19
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Sequence 134, Application US/09081385 Patent No. 6593456

RESULT 3 US-09-081-385-134

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Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity, and Methods
of Use Thereof
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Pacquence 77, Application US/08171718

Pactent No. 5707863

GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: Guesla, James F.
TITLE OF INVENTION: Therof
TITLE OF INVENTION: Therof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., Suite 600 STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                      STATE: CA
COMPUTRY: USA
ZIP: 94304-1018
COMPUTRY: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TRESTON TO WINDOWS
SOFTWARE: Fast SEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
FILING DATE: OS-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WU, Frank
REGISTRATION NUMBER: 41,386
REFERENCEY/DOCKET NUMBER: 22000-20577.21
TELECOMMUTCATION INFORMATION:
TELEPHONE: 650-813-5600
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: Of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
COMMENT OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 TCTTGCAGGAAGCGGC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
DEDNESS: single
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic
STRANDEDNESS:
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TOPOLOGY:
US-09-081-385-134
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Geguence 79, Application US/09135020

Factor No. 6274332

GENERAL INFORMATION:

APPLICANT: Reating, Mark T.

APPLICANT: Sanguinetti, Michael C.

APPLICANT: Splawski, Igor

TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH

TITLE OF INVENTION: ACAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION: KCNEI AS AN LQT GENE

TITLE OF INVENTION: WUMBER: US/09/135,020

CURRENT APPLICATION NUMBER: US/09/135,020

CURRENT FILING DATE: 1998-08-17

EARLIER FILING DATE: 1995-108-29

EARLIER APPLICATION NUMBER: 08/739,383

EARLIER APPLICATION NUMBER: 60/019,014

EARLIER APPLICATION NUMBER: 60/019,014

EARLIER FILING DATE: 1995-10-22

EARLIER FILING DATE: 1995-10-22

EARLIER FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFFWARER: PATENTING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SOFFWARER: PATENTING DATE: 1998-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 6e+03;
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Pred. No. 6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB1993
RICOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR.1993
ATTORNEY, AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
FREFRENCE/DOCKET NUMBER: 0609.38500
FILEBRANG/CATION INFORMATION:
TELEPRONG (202) 371-2600
FILEBRAY: (202) 371-2600
FILEBRAY: (202) 371-2540
FILERAX: 
                                                                                                                                                                                                                                                                                                                                0609.3850003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-135-010A-79/c
; Sequence 79, Application US/09135010A
; Patent No. 6277978
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92.9%;
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US-09-135-020-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Matches 13: Conserve
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US-09-135-020-79/c
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LENGTH: 20
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APPLICANT: Trofatter, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: MacCollin, Mia M.
APPLICANT: Guesla, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterner, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB 1; Length 20;
Pred. No. 6e+03;
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/111,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
PURASIFICATION DATA:
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
FILING DATE: 25-FEB-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
APPLICATION NUMBER: 0609.3850003
FELECOMMUNICATION NUMBER: 0609.3850003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAKX: (202) 371-2600
TELEFAX: (202) 371-2540
INPORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                             APPLICATION NUMBER: US/08/171,718
FILING DATE: 22-DEC-1993
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 77, Application US/08478087
Patent No. 6077685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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US-08-478-087-77/c
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US-09-597-735-79/c
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APPLICANT: Sagaulinetti, Michael C.
APPLICANT: Sagaulinetti, Michael C.
APPLICANT: Sagaulinetti, Michael C.
APPLICANT: Salawaki, 1gor
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ESTABLISHING
TITLE OF INVENTION: KCNEI AS N. LQT GENE
TILE REFERENCE: 2123-131
CURRENT APPLICATION NUMBER: US/09/444,871
CURRENT FILING DATE: 1999-11-22
EARLIER FILING DATE: 1999-10-3
EARLIER PELING DATE: 1996-10-3
EARLIER PELING DATE: 1995-12-22
EARLIER PELING DATE: 1995-12-22
EARLIER PELING DATE: 1995-12-22
EARLIER PELING DATE: 1995-12-22
EARLIER PILING DATE: 1995-12-22
EARLIER PILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 114
SEQ ID NO 99
SEQ ID NO 79
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%; Score 12.4; DB 3; Length 20; 92.9%; Pred. No. 6e+03; tive 0; Mismatches 1; Indels
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Connors, Timothy M.
APPLICANT: Connors, Timothy D.
APPLICANT: Burn, Timothy C.
APPLICANT: Splawski, 120.
ITILE REFERENCE: 2323-133
FURRENT FILING DATE: 1998-08-17
FRIOR APPLICATION NUMBER: 06/094,477
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR APPLICATION NUMBER: 08/921,068
FRIOR APPLICATION NUMBER: 08/739,383
FRIOR APPLICATION NUMBER: 08/739,383
FRIOR APPLICATION NUMBER: 06/019,014
FRIOR APPLICATION NUMBER: 06/019,014
FRIOR APPLICATION NUMBER: 06/019,014
FRIOR FILING DATE: 1995-12-22
KNUMBER OF SEQ ID NOS: 116
SEQ ID NO 79
FRIOR FILING DATE: 1995-12-22
INWHABER OF SEQ ID NOS: 116
ILENGTH: 20
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US-09-444-871-79/C
'Sequence 79, Application US/0944871
'Patrent No. 6329026
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Best Local Similarity 92.99
Matches 13; Conservative
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CORGANISM: Homo sapiens
US-09-444-871-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-135-010A-79
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Sequence 8114, Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GI, Yizhon
APPLICANT: PENN, Sharron G.
APPLICANT: HANZE, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ASSOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE KEFEKENCE: AEOMICA-7

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

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PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
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5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.4; DB
Pred. No. 6e+03
0; Mismatches
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                                  PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 08/921,068
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 08/739,383
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR APPLICATION NUMBER: 60/019,014
PRIOR APPLICATION NUMBER: 1995-12-22
NUMBER OF SEQ ID NOS: 116
2000-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                  Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
, ORGANISM: Homo sapiens
US-09-597-731-79
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US-09-866-108A-8114
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SEQ ID NO 79
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Pred. No. 6e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                Score 12.4; DB 3; Length 20;
Pred. No. 6e+03;
0; Mismatches 1; Indels
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PPLICANT: Splawski, Igor
ITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROWE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Carran, Michael C.
APPLICANT: Curran, Michael C.
APPLICANT: Curran, Timothy D.
APPLICANT: Connors, Timothy D.
APPLICANT: Splawski, Igor
APPLICANT: Splawski, Igor
TITLE OF INVENTION: KYLOTI - A LONG OT SYNDROME GENE
FILE REFERENCE: 2323-133
                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE KEFEKKUCK: 1232-1133
CURRENT PEDLICATION NUMBER: US/09/597,732
CURRENT FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/135,010
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 116
SOFFWARE: PATENTIN VET. 2.0
SEDENTH: 20
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Patent No. 6451534
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Sanguinetti, Michael
Curran, Mark B.
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Connors, Timothy D.
Burn, Timothy C.
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92.9%;
                                                                                                                                                                                   Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 92.5.
Local Similarity 92.5.
Conservative
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; ORGANISM: Homo sapiens
US-09-597-732-79
                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-09-444-295-79
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APPLICANT: Keating,
APPLICANT: Sanguine
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         SEQ ID NO 79
LENGTH: 20
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Sequence 130, Application US/09487445

Patent No. 6258600

GENERAL INFORMATION:
APPLICANT: Hong JOHNER COMBERT

TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION FILE REFERENCE: FTS-0107

CURRENT APPLICATION NUMBER: US/09/487,445

CURRENT FILING DATE: 2000-01-19

NUMBER OF SEQ ID NOS: 176

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.0%; Score 11.8; DB 3; 86.7%; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
, OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-445-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, KAMRIN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: LBL-
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (415) 705-8410
                 20 cacrrrrccacraaccacar
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MOLECULE TYPE: DNA (genomic)
US-08-534-479-1
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACTCTTGCAGGAAG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 base pairs
IYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                          RESULT 16
US-09-487-445-130/c
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US-09-422-978-8500/c

Sequence 8500, Application US/09422978

Sequence 8500, Application US/09422978

Sequence 8500, Application US/09422978

GENERAL INFORMATION:

APPLICANT: Chumakov. IJya

APPLICANT: Chumakov. IJya

TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

FILE REFERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1999-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-11-23

SARILER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 8500

LENGTH: 20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Robbins, Joan M.
APPLICANT: Trife, Richard
TITLE OF INVENTION: SKIN AND EYE DISEASES
TITLE OF INVENTION: SKIN AND EYE DISEASES
TITLE OF INVENTION: SKIN AND EYE DISEASES
CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-110-25
NUMBER OF SEQ ID NOS: 4523
SEQ ID NO 1380
LENGTH: 19
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                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%; Score 12; DB 4; Length 20; 75.0%; Pred. No. 9.6e+03; trive 0; Mismatches 5; Indels
82.4%; Pred. No. 7.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Cdk-we-hu ribozyme binding site US-09-696-791-1380
                                                                                                                                                                                                                             Sequence 1380, Application US/09696791
Patent No. 6770633
                                                                      4 TCTTGCAGGAAGCGGCT 20
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Best Local Similarity 75.0
Matches 15; Conservative
                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
  Best Local Similarity
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US-09-696-791-1380/c
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                        Matches
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                                                                                                                                APPLICANT: Christenson, Brik
APPLICANT: Christenson, Anthony J
APPLICANT: Coddman, Phyllis S
APPLICANT: DeMaggio, Anthony J
APPLICANT: DeCoddman, Phyllis S
APPLICANT: McElligott, David L
TITLE OF INVENTION: Human Poly (ADP-Ribose) Polymerase 2 Materials and
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION WIMBER: US/09/596,248D
CURRENT APPLICATION NUMBER: US/09/596,248D
CURRENT FILING DATE: 1999-06-16
NUMBER: PRIOR FILING DATE: 1999-06-16
NUMBER: PATERING DATE: 1999-06-16
NUMBER: PATERING DATE: 1999-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.0%; Score 11.6; DB 4; Length 20; 77.8%; Pred. No. 1.5e+04; Live 0; Mismatches 4; Indels
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APPLICANT: Walter, Funk D.
APPLICANT: Mieczyalaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REPERENCE: 080/003C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT PEPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PATENTIN VEXBION 3.1
SOFTWARE: PATENTIN VEXBION 3.1
SEQ ID NO 29
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/09972115A Patent No. 6599728 GENERAL INFORMATION: APPLICANT: Geron Corporation
                                                            Sequence 39, Application US/09596248D Patent No. 6599727 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACTCTTGCAGGAAGCGG 18
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8
Matches 14; Conservative
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Matches 14, Conserv
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US-09-972-115A-29
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                                              US-09-596-248D-39
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LENGTH: 20
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Sequence 49, Application US/09489869A

BENERAL INFORMATION:
APPLICANT: Susan Murray
APPLICANT: Lex M. Cowsert
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF MACROPHAGE MIGRATION INHIBITORY FACTOR
FILE REFERENCE: RTS-0110
CURRENT APPLICATION NUMBER: US/09/489,869A
NUMBER OF SEQ ID NOS: 88

SEQ ID NO 49
LENGTH: 20
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| Sequence 38. Application US/09596248D
| Patent No. 6599727
| GENERAL INFORMATION:
| APPLICANT: Christenson, Erik
| APPLICANT: Christenson, Erik
| APPLICANT: Devaggio, Anthony J
| APPLICANT: Goldman, Phyllis S
| APPLICANT: McElligott, David L
| TITLE OF INVENTION: Methods
| TITLE OF INVENTION: Methods
| TITLE OF INVENTION: Methods
| TILE REFERENCE: 27866/36544
| CURRENT APPLICATION NUMBER: US/09/596,248D
| CURRENT APPLICATION NUMBER: 60/139,543
| PRIOR FILING DATE: 1999-06-16
| NUMBER OF SEQ ID NOS: 68
| SEQ ID NO 38
| LENGTH: 20
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Query Match 58.0%; Score 11.6; DB 2; Length 20; Best Local Similarity 77.8%; Pred. No. 1.5e+04; Matches 14; Conservative 0; Mismatches 4; Indels
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Pred. No. 1.5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.0%; Score 11.6; I
Best Local Similarity 77.8%; Pred. No. 1.5s
Matches 14; Conservative 0; Mismatches
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US-09-489-869-49/C
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GB 24263.6

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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: JI, Yonggang
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: ASOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLE REFERENCE: AEOMICA-7

CURRENT PAPLICATION NUMBER: US/09/866,108A

CURRENT PILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-01-0-04

PRIOR PILING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30
                                                                                                                                                                                                                                                   APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE FILE REFERENCE: AEOMICA-7
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0; Mismatches 1
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
              Sequence 115, Application US/09866108A
Patent No. 6686188
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                                                                                                 GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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Matches 12; Conservative
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US-09-866-108A-116
US-09-866-108A-115
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PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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Pred. No. 1.9e+04;
); Mismatches 1; Indels
LING DATE: 2000-10-04
PLICATION NUMBER: US 60/236,359
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Best Local Similarity 92.5-
Best Local 2; Conservative
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Homo sapiens
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APPLICANT: GU, Yizhong
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
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NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
PARTON NO. 6686188
SEQ ID NO 118
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARB: Aeomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 117
LENGTH: 17
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Pred. No. 1.9e+04;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 118, Application US/09866108A Patent No. 6686188 GENERAL INFORMATION:
APPLICANT: GU, Yizhong APPLICANT: JI, Yonggang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.0%;
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Best Local Similarity 92.3%;
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                              ORGANISM: Homo sapiens
US-09-866-108A-117
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APPLICANT: HANZEL, DAYLG K.
APPLICANT: HANZEL, DAYLG K.
APPLICANT: CHEN, Wensheng
APPLICANT: GHENGON, MAIK
TITLE OF INVENTION, MAIK
TITLE OF INVENTION, MAIK
TITLE OF INVENTION WASIR: US 60/207,456
FILE REFERENCE: 2000-05-26
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR FILING 
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 1.9e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/207,456
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209-866-108A-6215/c
; Sequence 6215, Application US/09866108A
; Patent No. 6686188
Sequence 119, Application US/09866108A Patent No. 668618B
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PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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Best Local Similarity 92.3
Best Local Similarity 92.3
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APPLICANT: SHANNOW, MARK

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REPERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR PAPPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-36
PRIOR PAPPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-10-37
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR PELING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Acomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 6216
LENGTH: 17
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Pred. No. 1.9e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-866-108A-6217/c
; Sequence 6217, Application US/09866108A
; Patent No. 6686188
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACTCTTGCAGGA 13
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Best Local Similarity 92.3
Matches 12; Conservative
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CORGANISM: Homo sapiens
US-09-866-108A-6217
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-866-108A-6216
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Best Local Similarity
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US-09-866-108A-6216/C
US-09-866-108A-6216/C
Sequence 6216, Application US/09866108A
Sequence 6216, Application US/09866108A
GENERAL INFORMATION:
APPLICANT: GT, Yizhong
APPLICANT: PRNK, Sharron G,
APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICANT
FILE REFERENCE: AEOMICAN
              PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-09-27

PRIOR PLICATION NUMBER: US 66/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR PLICATION NUMBER: PCT/USO1/00666

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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CURRENT PELING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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APPLICATION NUMBER: US 60/207,456
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APPLICANT: HANZEL, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANKAN, Mark
APPLICANT: SHANKANSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
TITLE OF INVENTION: WASSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
CURRENT FILING DATE: 2000-05-25
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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PRIOR PRINCE PRINC
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US-09-866-108A-6219/C
; Sequence 6219, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: UI, Yizhong
; APPLICANT: PENN, Sharron G.
; APPLICANT: RANK, David K.
; APPLICANT: RANK, David K.
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION
TITLE OF INVENTION: ANTISENSE
CURRENT APPLICATION UNBER: US/09/256,496
CURRENT FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 10
LENGTH: 18
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Pred. No. 1.9e+04;
); Mismatches 1;
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Pred. No. 1.9e+04;
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Patent No. 6686188
SEQ ID NO 6219
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US-09-517-584A-11/c
; Sequence 11, Application US/09517584A
; Patent No. 6187587
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09256496; Patent No. 5998206; GENERAL INFORMATION:
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Best Local Similarity 92.3
Matches 12; Conservative
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Best Local Similarity
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; ORGANISM: Homo (
US-09-866-108A-6219
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Sequence 6247, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
GURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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US-09-856-662-20
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Patent No. 6790616
GENERAL INFORMATION:
APPLICANT: MORIBE, TOYOKi et al.
ITILE OF INTENTION: Method for typing HLA class 1 genes
FILE REFERENCE: 0032-0261P
CURRENT APPLICATION NUMBER: US/09/856,662
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 1998-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.0%; Score 11.4; DB 4; 92.3%; Pred. No. 1.9e+04; tive 0; Mismatches 1;
                                                                                                               Best Local Similarity 92.3%; Pred. No. 1.98+04; Matches 12; Conservative 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 38
US-09-474-432B-429
Sequence 429, Application US/09474432B
Parent No. 6528640
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA; Chlamydia pneumoniae; ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 16
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                                                                                                                                                                                    4 TCTTGCAGGAAGC 16
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Best Local Similarity 92.3
Matches 12; Conservative
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us-10-773-6

APPLICANT: Vickie L. Brown-Driver
APPLICANT: Lex M. Cowert
ITLE OF INVENTION:
PILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/517,584A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS:
SEQ ID NO 11
LENGTH: 20
TYPE: 20
TYPE: 20
TYPE: 20
TYPE: 20
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Sequence 27, Application US/09467082

GENERAL INFORMATION:
APPLICANT: Bret P. Monia
APPLICANT: Lex M. Cowmert
TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
FILE REFERENCE: RTS-0088
CURRENT APPLICATION NUMBER: US/09/467,082
CURRENT PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 27
LENGTH: 20
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Sequence 51, Application US/09658687A

Sequence 51, Application US/09658687A

Patent No. 6387699

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

TILE CO INVENTION: AVAISENSE MODULATION OF A20 EXPRESSION

TILE REFERENCE: RTS-0141

CURRENT APPLICATION: NUMBER: US/09/658,687A

CURRENT FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 51

LENGTH: 20
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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57.0%; Score 11.4; DB 3;
Best Local Similarity 92.3%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 1;
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-082-27
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; OTHER INFORMATION: Antisense Oligonucleotide
US-09-658-687A-51
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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GENERAL INFORMATION:
APPLICANT: GU, Yongqang
APPLICANT: GU, Yongqang
APPLICANT: GU, Yongqang
APPLICANT: GU, Yongqang
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: AMAK, David R.
APPLICANT: STANNON, MATA
TILLE REFERENCE: AECMICA-2
FILE REFERENCE: AECMICA-2
FILE REFERENCE: AECMICA-2
FILE REFERENCE: AECMICA-2
FILE REFERENCE: AECMICA-2
FRICA PLILING DATE: 2000-05-26
FRICA PAPLICATION NUMBER: US 60/207,456
FRICA PLILING DATE: 2000-05-26
FRICA PLILING DATE: 2000-05-26
FRICA PLILING DATE: 2000-05-26
FRICA PLILING DATE: 2000-05-26
FRICA PLILING DATE: 2001-00-4
FRICA PLILING DATE: 2001-01-04
FRICA PLILING DATE: 2001-01-30
FRICA PLILING DATE: 2001-01-30
FRICA PLILING DATE: 2001-01-30
FRICA FLILING DATE: 2001-01-30
FRICA FRICA APPLICATION NUMBER: PCT/USO1/00669
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FRICA FRICA
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Pred. No. 2.4e+04;
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Patent No. 6686188
SEQ ID NO 7632
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; Sequence 7632, Application US/09866108A
; Patent No. 6686188
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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                                                                                 APPLICANT: Karpeisky, Anex
APPLICANT: Karpeisky, Alex
APPLICANT: Seedlear, David
APPLICANT: Sweedlear, David
APPLICANT: Sweedlear, David
APPLICANT: Sweedlear, David
APPLICANT: School, Shawn
ITILE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REPERENCE: MBHB00-831-B (247/276)
FURRENT APPLICATION NUMBER: US 60/084,866
FRIOR APPLICATION NUMBER: US 60/084,727
FRIOR FILING DATE: 1998-04-29
FRIOR FILING DATE: 1998-11-04
FRIOR FILING DATE: 1998-11-04
FRIOR FILING DATE: 1999-11-04
FRIOR FILING DATE: 1999-11-04
FRIOR FILING DATE: 1999-11-04
FRIOR FILING DATE: 1999-12-04
FRIOR FILING DATE: 1999-1301,511
FRIOR FILING DATE: 1999-14-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
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APPLICANT: Beaudry, Amber
APPLICANT: Rarpeisky, Alex
APPLICANT: Karpeisky, Alex
APPLICANT: Admic, Jasenka Matulic
APPLICANT: Sweedler, Dasenka Matulic
APPLICANT: Sweedler, Dasenka Matulic
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: NUCLeotide Triphosphate and their Incorporation into Oligonucleot
CURRENT APPLICATION NUMBER: US/09/476,387
CURRENT FILING DATE: 2001-04-04
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Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
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PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR PELING DATE: 1999-12-29
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-11-04
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PRIOR PELING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 1524
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LENGTH: 17
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Matches 11; Conservative
Beigelman, Leo
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US-09-474-432B-429
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Aas96785 Human STA
Adm14825 Human mPG
Aaf46590 IGFBP3 01
Aaf46590 IGFBP3 01
Aaf46589 IGFBP3 01
Adm92376 Pancreati
Adm14384 Human mPG
Adm14384 Human mPG
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Aat90721 Human KVL
Aat91069 Human KVL
Aaz90745 Human KVL
Aaz9875 Mutant hu
Adr72365 Antisense
Adr72397 Antisense
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Ade34379 Reverse p
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                              GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antisense compound (1), 8 to 30
nucleobases in length, that is targeted to a nucleic acid molecule
encoding STAT3 (Signal Transducer and Activator of Transcription) and
which inhibits the expression of it. (1) has antinflammatory,
antirheumatic, cytostatic and immunostimulatory activities. (1) is used
for inhibiting the expression of STAT3 in cells or tissues, treating an
animal having a disease or condition associated with STAT3 or a human
chaving a disease or condition characterised by a reduction in apoptosis,
and inducing apoptosis in a cell. Diseases or conditions that are treated
and/or neck, leukaemia, myeloma, melanome or lymphoma. (1) can also be
used for diagnostic methods in detecting and determining the role of
STAT3 in various cell functions, physiological processes and conditions
and for diagnosing the conditions associated with expression of STAT3.
(1) can be used alone or with other drugs as an immunostimulator. (1) is
used in sandwich and colourimetric assays, involving enzyme conjugation
and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
STAT3 and AAC93231 encodes mouse STAT3 to AAC93150 encodes human
CHAPTS and ACC92231 encodes mouse STAT3 to AAC93150 encodes human
                        Aax57670 Human G-a
Aax96921 PCR prime
Aac72420 Single nu
Aaa54448 Primer fo
Aaf91296 Human E2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense compound for inhibiting the expression of signal transducer and activator of transcription 3 (STAT3) in cells or tissues and treating diseases or condition associated with STAT3, such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention. AAC93151 to AAC93230 and AAC93234 to AAC932300 represent STAT3 phosphorothioate antisense oligomucleotides, and AAC93300 represents a mismatch control oligomucleotide which are used in example
  Acn69314 Human GDM
Acn63214 Human GDM
                                                                                                                                                                                                                                                                                         Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide; modulation; signal transducer and activator of transcription; DNA-binding protein; signal transduction; inhibition; apoptosis; inflammatory disease; cancer; antiinflammatory; antirheumatic; cytostatic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma; melanoma; lymphoma; diagnosis; ss.
                                                                                                                                                                                                                                                                    Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.
                                                                                                                        ALIGNMENTS
            ACN63214
AAZ57670
AAX96921
AAC72420
AAA5448
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                                                                                                                                                                                        AAC93168 standard; DNA; 20 BP
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The invention relates to antisense compounds targeted to a nucleic acid molecule encoding a signal transducer and activator of transcription (STAT) protein, specifically STAT3, where the antisense compounds inhibit the expression of STAT3. The antisense sequences are useful for inhibiting the expression of STAT3 in cells or tissues, inducing Fasnediated apoptosis in cells, and sensitising cells to apoptosis. They are also useful for treating an animal having a disease or condition foreast, prostate with STAT3. These disorders include inflammatory or autoimmune disease, particularly rheumatoid arthritis, cancers, such as those of the breast, prostate, brain and head and neck and leukaemias, myelomas, melanomas and lymphomas. Also treatable are human diseases or conditions characterised by a reduction in apoptosis or an insensitivity to apoptotic signals. The sequences of the invention can be used in clinical apoptotic signals.
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STAT3; human; signal transducer and activator of transcription; ss; STAT; antisense gene therapy; Fas-mediated apoptosis; inflammatory disease; autoimmune disease; theumatoid arthritis; cancer; breast; prostate; head; neck; briain; leukaemia; myeloma; melanoma; lymphoma; apoptosis; antiinflammatory; immunosuppressive; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                research, for detecting and determining the role of STAT3 in various cell functions and physiological processes and for diagnosing conditions associated with the expression of STAT3. The sequences represent cDNA encoding human STAT3 and human STAT3 oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antisense compound useful for treating and diagnosing inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases and cancers, is targeted to a nucleic acid molecule encoding signal transducer and activator of transcription proteins.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.
                                                                                                                                             ;;
0
                                                                        Length 20;
                                                                                                                                          0; Indels
Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                 Score 14; DB 3; Lk
Pred. No. 5.5e+03;
7; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 13; 21pp; English.
                                                                            70.0%; FIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JAN-2001; 2001US-00758881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1999; 99US-00288461.
06-APR-2000; 2000WO-US009054
                                                                        70.08;
                                                                                                                                                                                                               1 GACTCTTGCAGGAA 14
                                                                                                                                                                                                                                                                                    7 GACTCTTGCAGGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS96785 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KARR/) KARRAS J G.
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2001029250-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Karras JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS96785;
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us-10-773-678-342.max.rng

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1 GACTCTTGCAGGAAGCGGCT 20
                                                                                                                                                                                                                                                      GATTCCTGCACGAAGTGGCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0140345P.
                                                                                                                                                                                                                                                                                                               AAF46591 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                IGFBP3 oligonucleotide #11.
                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001 (first entry)
                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-041421/05.
                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200078341-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-2000.
                                                                                                                                                                                                                                                                                                                                     AAF46591;
                                                                                                                                                                                                                                                        20
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                          RESULT 4
AAF46591/c
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                                                                                                                                                                                                                      chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; antidandin E2 synthase; mPGES-1; mPGES-1 inhibitor; antidancorseaglandin E2 synthase; inhibitor; cytostatic; antidiabetic; immunoomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; antianflammatory; neuroprotective; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiavascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prosteglandin E2 synthese (mPCSS-1). The human mPGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds,
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     /mod_base= OTHER
/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
                                                                                                                                                                                                   Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
                                 ;
            Length 20;
          / Match 70.0%; Score 14; DB 6; Length 20; Local Similarity 100.0%; Pred. No. 5.5e+03; les 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'mod_base= OTHER
'note= "2'-0-methocyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 1012; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        base= OTHER
                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2002; 2002US-0413549P.
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                                                                                                                                  ADM14825 standard; DNA; 20
                                                      1 GACTCTTGCAGGAA 14
                                                                          7 GACTCTTGCAGGAA 20
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                                                                                                                                                                              (first entry)
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-305094/28.
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                                                                                                                                                                                                                                                                                                                                                                        Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                       modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_base
                                                                                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                              01-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gierse JK;
                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischemia.
                                                                                                                                                        ADM14825;
             Query Match
                                                                                                                        ADM14825/c
                                                                                                                                                                                                                                                                                                                                       Ношо
                                 Matches
                                                                                                              RESULT 3
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having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tisques; and (3) a method of treating an animal having a disease or condition associated with mPGES-1. MPGES-1 chimeric antisquencic, immunomodulator, cardant, neuroprotective, antidiabetic, immunomodulator, cardant, neuroprotective, ophthalmatory, neuroprotective, nootropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBPB), which is capable of inhibiting or reducing growth factor mediated cell proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 13.6; DB 12; Length 20; 80.0%; Pred. No. 8.6e+03; ive 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wraight CJ, Werther GA, Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 44; 201pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
inflammation and/or other disorders. The present sequence is an oligonuclectide which can be used to design the antisense oligonuclectides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 13; DB 4; Length 15; 100.0%; Pred. No. 1.7e+04; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Seguence 15 BP; 1 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edmondson SR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF46590 standard; DNA; 15 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0140345P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GCAGGAAGCGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGGAAGCGGCT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-041421/05.
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200078341-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1999;
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         8888888888888
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δ g The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-INE Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used odesign the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-F45161). The method is useful for ameliorating the effects of psoriasis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense therapy; antiproliferative; antinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding proctein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasta; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasis; kidney disease; neovascular condition; hyperplasis; kidney disease;
ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood
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0
                                                                                                                                                                                           65.0%; Score 13; DB 4; Length 15; 100.0%; Pred. No. 1.7e+04; tive 0; Mismatches 0; Indels
                                                                                                                                                      Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wraight CJ, Werther GA, Edmondson SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 44; 201pp; English.
                                                                                                                vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2000; 2000WO-AU000693
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF46589 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGFBP3 oligonucleotide #9.
                                                                                                                                                                                                                                                                                 8 GCAGGAAGCGGCT 20
                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                            GCAGGAAGCGGCT 2
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                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF46589;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               AAF46589/c
                                                                                                                                                                                                                                         Matches
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WPI; 2004-305094/28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM14384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for diagnosing pancreatic cancer (PNC) or a predisposition to developing PNC in a subject. The method comprises determining a level of expression of a PNC-associated gene in a patient derived biological sample, where an increase or decrease of the level compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing PNC. Also described: (1) a PNC reference expression profile, comprising a pattern of gene expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (2) a method of screening for a compound for treating or preventing PNC or malignant PNC; (3) a kit comprising a detection reagent which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906 or the encoded polypeptides; (4) an array comprising two or more nucleic acids which bind to one or more nucleic acids equences; i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a composition, for treating or preventing PNC; comprising a pharmaceutical amount of: (a) an antisense polynucleotide or small interfering NNA against a method of treating or preventing PNC 606-640 and PNC 682-741 or PNC 850-87 any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-87 any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic cancer; diagnosis; pancreatic cancer-associated gene; cytostatic; vaccine; gene therapy; human; reverse transcription; PCR; primer; ss; semi-quantitative RT-PCR experiment.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing pancreatic cancer (PNC) comprises determining a level of expression of a PNC-associated gene in a patient derived biological
disease, kidney disease, hyperproliferation of the inside of blood
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                                                                                               Query Match 65.0%; Score 13; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 1.7e+04; Matches 13; Conservative 0; Mismatches 0; Indels
                                                            Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 13; 152pp; English.
                       vessels or any other hyperplasia
                                                                                                                                                                                                                                                                                                                                    ADM92376 standard; DNA; 20 BP.
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28-FEB-2003; 2003US-0450889P
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                                                                                                                                                                                     8 GCAGGAAGCGGCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-330205/30.
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Synthetic.
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ingredient and a pharmaceutical carrier; and (7) a method of predicting recurrence of PNC. The compounds have cytostatic activity, and can be used in vaccines and in gene therapy. The method is useful in diagnosing PNC or a predisposition to developing PNC in a subject. The methods, compounds and compositions are useful in treating or preventing PNC. The polypeptides are useful as vaccines against PNC. The present sequence represents a reverse transcription (RT) PCR primer used in semi-quantities RT-PCR experiments related to the diagnosis of PNC, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.6; DB 12; Length 20; Pred. No. 2.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                         used in an example from the present invention.
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/mod_base= OTHER
/note= "2'-O-methocyethyls"
16 .20
/*tag= C
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/mod_base= OTHER
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to 9434.3. The present invention also describes: (1) antisense compounds, having a sequence comprising 8-30 bp targeted to a nucleic acid encoding mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and of inhibiting the expression of antisense oligonucleotides and antisense compounds have cytostatic, antisanse oligonucleotides and antisense compounds have cytostatic, antidiabetic, immunomodulator, cardiant, neuroprotective, antinflammatory, neuroprotective, neuroprotective, copthalmological, immunomodulatory and cardiavascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's condition associated with mPGES-1 e.g., inflammation, Alzheimer's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytosetatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; notropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer; disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or ophthalmic, immunological, cardiovascular or neurological disorder.
               New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
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/note= "2'-O-methocyethyls"
                                                                                                                          Claim 4; SEQ ID NO 571; 132pp; English.
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Best Local Similarity 78.9
Matches 15, Conservative
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Synthetic.
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                                                                                    ischemia.
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mpGES-1). The human mpGES-1 gene is located on chromosome 9, more specifically to offer mpGES-1, which specifically they are more in a tribibite a sequence comprising 8-30 bp targeted to a nucleic acid encoding mpGES-1, which specifically hybridise with the nucleic acid encoding inhibites its expression; (2) a method of inhibiting the expression of mpGES-1 in cells or tissues; and (3) a method of treating an animal having a disease or condition associated with mpGES-1. MpGES-1 chimeric antidiabetic, immunomodulator, cardiant, neuroprotective, cantidiabetic, immunomodulator, cardiant, neuroprotective, notropic, antiarthritic, vasotropic, ophthalmological, immunomodulatory and cardiovascular activities, and can be used as mpGES-1 inhibitors and in gene therapy. The antisense compound con the used as mpGES-1 inhibitors and in gene therapy. The antisense compound confict on associated with mpGES-1 e.g., inflammation, Alzheimer's condition associated with mpGES-1 e.g., inflammation, Alzheimer's ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss; primer; probe; tumour suppression; tumour reversion; apoptosis; virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
                                                                                                                                                                                                                                                                                                                   New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 12.6; DB 12; 78.9%; Pred. No. 2.6e+04; tive 0; Mismatches 4;
/mod_base= OTHER
/note= "2'-O-methoxyethyls"
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 1013; 132pp; English.
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tes 15; Conservative
                                                                                                                                                                                                          (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                WPI; 2004-305094/28.
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                                                        WO2004028458-A2
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                                                                                             08-APR-2004.
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                                                                                                                                                                                                                                               Gierse JK;
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                                                                                                                                                                                                                                                                                                                                                                             ischemia.
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Matches
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ADB45311
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Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis instrected; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking
                                                                                                                                                                                                                                                                                                                                                                  with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                            This sequence represents an isolated nucleic acid sequence associated
                                                                                                                                                                      New nucleic acid sequences associated with tumor suppression, regres apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 62.0%; Score 12.4; DB 10; Length 17; Local Similarity 92.9%; Pred. No. 3.3e+04; les 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP specific lower PCR primer SEQ ID 2566.
                                                                          Tuijnder M, Telerman A, Amson R;
                                                                                                                                                                                                                                                                                       Claim 1; Page 311; 798pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 63; 83pp; English.
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                      (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH39770 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 TGCAGGAAGCGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 rccaegaaeceecr 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-290930/30
                                                                                                                            WPI; 2003-250498/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH39770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH39770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragments of at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 15 consecutive nucleotides of these nucleotides, a sequence having at least 80% identity, after optimal alignment, with the nucleotides, or the complement, or corresponding RNA, of the nucleotides. The nucleotides are used as probes or primers for detecting, identifying and/or amplifying nucleic acids, as in vitro sense and antisense sequences, of nucleotides involved in tumour suppression or reversion, apoptosis and or viral resistance, to produce recombnant polypeptides, and to prepare transgenic animals, as experimental models. The nucleotides (also vectors containing them and cells containing the vectors), the encoded polypeptides and antibodies of viral infections or diseases characterized by development of tumours or viral infections or diseases characterized by development of tumours or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

Analysis of the expression of the nucleotides can be used for diagnosis also be used to screen for their specific interactive molecules.

Conduct of the septemble of the sequence of the nucleotides and polypeptides can be used to screen for their specific interactive molecules.
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                                                                                                                                                                                                                                                                                                        New nucleic acid encoding human prostate membrane-specific antigen, useful e.g. for treatment of tumors and viral infection, also related polypeptide and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.4; DB 10;
Pred. No. 3.3e+04;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour suppressor sequence #1175.
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 690; 771pp; French.
                                                                                                                                                                                                                  Tuijnder M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression of the nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC52408 standard; DNA; 17 BP.
                                                                                                                                                             (MOLE-) MOLECULAR ENGINES LAB
                                                    17-SEP-2002; 2002WO-IB004219.
                                                                                                         17-SEP-2001; 2001FR-00011981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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                                                                                                                                                                                                                  Amson R,
                                                                                                                                                                                                                                                                 WPI; 2003-441574/41.
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                                                                                                                                                                                                               Telerman A,
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  15-MAY-2003
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Gaps

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cc sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the coligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for eightity of a SNP and for genotyping nucleic acid samples, for eightity of a SNP and for genotyping nucleic acid samples, for eightity of a snP passociation analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases eig.

Cc agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial diseases, including, rheumatoid arthritis, multiple sclerosis, including, rheumatoid arthritis, multiple sclerosis, incroorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inspecting genetic susceptibility of Helicobacter pylori- related gastric carcinoma by checking Lewis blood-type antigen-associated gene polymorphism, applicable in screening individuals with high risk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori; gastric carcinoma; Lewis antigen; polymorphism; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for inspecting the genetic susceptibility of Helicobacter pylori related gastric carcinoma. The method of the invention comprises checking the polymorphism of the Lewis blood-type antigen-associated gene, with susceptibility particularly based on the recessive se allele and/or dominant homozygous Se/Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.0%; Score 12.4; DB 4; Length 18; 92.9%; Pred. No. 3.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 BP; 4 A; 4 C; 9 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYPE-) UNIV PEKING SCHOOL ONCOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ke Y, Jiang J, Ning T, Lu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE34379 standard; DNA; 18 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CTTGCAGGAAGCGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reverse primer P4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer; ss.
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The sequences given in AAQ71110-55 are primers which were used to amplify the 17 exons of the NPZ gene. NPZ is a neurofibromatosis which is characterised by bi-lateral schwannomas. The NPZ "gene" has been shown by linkage studies to be assigned to chromosome 22. The missing or mutated gene in NPZ patients has been shown to be the merlin gene. The gene encodes a protein, merlin (moesin-ezin-radixin-like protein), which possesses tumour suppressor activity, and whose tumour suppressor activity, and whose tumour suppressor activity and whose tumour suppressor activity and makers bill and bill be on chromosome 22 between the known markers bills!

Decided to a mutant suppressor activity and whose tumour suppressor mutated in which a gene in which a gene in which a
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genotype. The method is applicable in screening individuals with high risk and in a follow-up survey for intervention, prevention and early diagnosis. In an experiment from the invention the Lewis gene fragments with TS9G, GS08A and T10G7A polymorphism sites for PCR amplification were obtained for use after extracting samples of peripheral lymphocyte DNA from subjects. The mutation was then identified for assessing disease risk and diagnosis. The current sequene represents a PCR primer for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma; sequence-tagged site assay; chromosome 22; NP2; deletion; hearing loss; neurofibromatosis; merlin; mosein-erzin-radixin-like protein; D2S28; tumour suppressor; activity; meningioma; cytoskeleton; gene therapy; merlin-associated tumour; D2S28; posterior capsular lens opacity; deafness; balance disorder; paralysis; ss.
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                            Length 18;
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                                                                                                                                                                                                           62.0%; Score 12.4; DB 12; 92.9%; Pred. No. 3.38+04; ative 0; Mismatches 1;
                                                                                                                                                                        Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                      amplification of a region of the Lewis gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ71136 standard; cDNA; 20 BP.
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93US-00026063.
93US-00108808.
93US-00171718.
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                                                                                                                                                                                                                                                                                     2 ACTCTTGCAGGAAG 15
                                                                                                                                                                                                                                                                                                                      ACTCTGGCAGGAAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                                                                              Local Similarity res 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-272992/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trofatter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP613945-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ71136;
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                  AAQ71136/c
                                                                                                                                                                                                                                                   Matches
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AAT91069 standard; DNA; 20
                                                                     AAT91069;
                                   AAT91069/c
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AAZ90745/
                        RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer 5 (AAT90721) and primer 6 (AAT90722) were designed to amplify DNA encoding the S4 region of human KVLQT1 (see AAW10038). PCR primers (AAT90717-28) were used in single-strand conformation analysis (SSCP) to define mutations in the human KVLQT1 gene (see AAT90730) associated with long QT syndrome (LQT). An initial SSCP identified an anomalous conformer in LQT-affected members of 6 large families. Further SSCP analyses identified a KVLQT1 intragenic deletion and 9 missense mutations associated with LQT in small families and sporadic cases
mutation of A to T at the first position of the codon encoding amino acid 220 causes the substitution of Tyr for Asn. The merlin gene may be used in gene therapy for the treatment of a merlin-associated tumour or NF2, or for prevention of schwannoma, maningioma, posterior capsular lens opacities, deafness or hearing loss, balance disorders or paralysis.
                                                                                                                                                                                                                                                                                                                                    KVLQT1; long QT syndrome; arrhythmia; mink; potassium channel; diagnosis; therapy; human; single strand conformation polymorphism; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human minK and Xenopus KVLQT1 coding sequences - used for assays for identifying drugs which can be used for preventing or treating long QT syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.0%; Score 12.4; DB 2; Length 20; 92.9%; Pred. No. 3.3e+04; ive 0; Mismatches 1; Indels
                                                                                                      Score 12.4; DB 2; Length 20;
Pred. No. 3.3e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                   Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
                                                           (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Curran ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 12; Page 44; 105pp; English.
                                                                                                                                                                                                                                                                                                                 Human KVLQT1 S4 region PCR primer 5.
                                                                                                                                                                                                                                           AAT90721 Standard; cDNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanguinetti MC,
                                                                                                          62.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0019014P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US019756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                        3 CTCTTGCAGGAAGC 16
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-402190/37.
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keating MT,
                                                                                                                                                                                                                                                                                          12-FEB-1998
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                                                                                                                                                                                                                                                                  AAT90721;
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                                                                                                                                  Matches
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PCR primer 5 (AAT91069) and primer 6 (AAT91070) were designed to amplify DNA encoding the S4 region of human KVLQT1 (see AAA33355). PCR primers (AAT91065-76) were used in single-strand conformation analysis (SSCP) to define mutations in the human KVLQT1 gene (see AAT94004) associated with long QT syndrome (LQT). An initial SSCP identified an anomalous conformer in LQT-affected members of 6 large familities. Further SSCP analyses identified a KVLQT1 intragenic deletion and 9 missense mutations associated with LQT in small families and sporadic cases
                                                                                 syndrome; arrhythmia; minK; potassium channel; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human potassium channel gene, KVLQT1, - used to develop products for diagnosis, prevention and therapy of long QT syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein; antiarrhythmic; gene therapy; human; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.0%; Score 12.4; DB 2; Length 20; 92.9%; Pred. No. 3.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Connors TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human KVLQT1 mutation defining primer 5.
                                           Human KVLQT1 S4 region PCR primer 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Page 44; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Landes GM,
                                                                                                                 therapy; human; PCR; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                         95US-0019014P.
                                                                                                                                                                                                                                                                                                                           96WO-US019917.
                                                                                                                                                                                                                                                                                                                                                                                               96US-00739383
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(GENZ ) GENZYME GENETICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 TGCAGGAAGCGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keating MF, Curran ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-402191/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                      KVLQT1; long
                                                                                                                                                                                                                                  WO9723632-A1
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                           20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                         22-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1996;
01-MAR-1998
                                                                                                                                                                                                                                                                                03-JUL-1997
                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ90745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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7 TGCAGGAAGCGGCT 20

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18 TGCAGGAAGCGGAT 5

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The invention relates to KVLQT1 nucleic acids which have a mutation compared to wild-type KVLQT1 (AAZ98901) The KVLQT1 gene encodes a protein of 676 amino acids which forms a cardiac I(ks) poteasium channel with the KCNE1 protein (AAY80563). The KVLQT1 gene contains 15 introns and encodes a protein containing 6 putative transmembrane segments and a pore forming region. The gene has been mapped to the chromosomal location 11p15.5. The sequences AAZ9891-129892 represent PGR primers used to diagnose mutations in the KVLQT1 gene. Mutations in the KVLQT1 or KCNLE1 genes result in cardiac arrhythmias observed as a prolonged QT curve in electrocardiograms (Long QT syndrome). The genes and proteins can be used for the diagnosis of subjects with long QT syndrome. They can also be used to screen for drugs which can be used for treating or preventing long QT syndrome. The KVLQT1 nucleic acids can be used for gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mod_base= OTHER
/mod_base= OTHER= phosphorothioate nucleotide. All cytosines
a/note= "OTHER= phosphorothioate nucleotide. All cytosines
a/note= Smethylcyldines. Residues 1 to 5 and 15 to 20 are
2'-methoxyethyl nucleotides."
                                            New isolated mutant KVLQT1 nucleic acids, useful for developing products for the diagnosis, prevention and treatment of long QT syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; kinesin-like 1; N2 kinesin; bimC kinesin; cellular proliferation; cancer; B-cell leukaemia; autoimmune disease; carpal tunnel syndxome; Raynaud's phenomenon; systemic sclerosis; Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis; systemic lupus erythematosus; human; ss; ISIS 344901; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligo targeted to human kinesin-like 1, ISIS 344901.
                                                                                                                                                                                                                                                                                                                                                                                                            Match 62.0%; Score 12.4; DB 3; Length 20; Local Similarity 92.9%; Pred. No. 3.3e+04; les 13; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                and KVLQTI peptides can be used for peptide therapy
                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                             Example 13; Page 78; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2003; 2003US-00714796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365/c
ADR72365 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TGCAGGAAGCGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 TGCAGGAAGCGGAT S
             WPI; 2000-195199/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004180847-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Rattus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
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                                                                                                                                                                                                                                                                                                                                                            The invention relates to KVLQT1 and KCNE1 genes, associated with long QT (LQT) syndrome. It provides a minK protein comprising a mutation which substitutes the wild type amino acids with Leu, Asp, Leu, Hisp and Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and treating LQT. The ability to predict LQT enables physicians to prevent the diseases with medical therapy such as beta blocking agents and opts for better treatments. Sequences AAZ30741-Z90752 represent PCR primers for defining human KVLQT1 mutations
                                                                                                                                                                                                                                                             Mutant forms of genes encoding minK protein and KVLQT1 protein involved in cardiac potassium channel formation useful for screening drugs, for preventing and treating cardiac arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss; cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy; chromosome 11p15.5; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant human long QT syndrome-associated KVLQT1 diagnostic primer 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connors TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.0%; Score 12.4; DB 3; Length 20; 92.9%; Pred. No. 3.3e+04; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curran ME, Landes GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                 Splawski I;
                                                                                                                                                                                                                                                                                                                                  Example 13; Page 75; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ98975 standard; DNA; 20 BP
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Burn TC, Splawski I;
                                                                                                                                                                                                 Sanguinetti MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TGCAGGAAGCGGCT 20
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                              WPI; 2000-195262/17.
                 WO200006600-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999;
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17-AUG-1998;
                                                                                 06-OCT-1998;
                                                                                                                29-JUL-1998;
                                                                                                                                 17-AUG-1998;
                                                                                                                                                                                                 Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-2000.
                                              10-FEB-2000
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Gaps

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The present invention relates to antisense compounds, compositions and methods for modulating the expression of kinesin-like 1. The superfamily of kinesins function as molecular engines to bind and transport vesicles and organelles along microtubules using energy supplied by ATP. Kinesin-like 1, a member of the NZ (also called bimC) family of kinesins, is involved in separating the chromosomes by directing their movement along microtubules in the bipolar spindle. Kinesin-like 1 is also known as KNSII, Egy. HRSE, KIFII, thyroid interacting protein 5 and TRIPS. Inhibition of kinesin-like 1 may be a target for arresting cellular cof kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, cof kinesin-like 1 systemic sclerosis, Sjorgren's syndrome, rheumatoid arbutisense nucleic acid oligomers, targeted to the gene concoding kinesin-like 1. Also provided are methods of screening for modulators of kinesin-like 1. Aleast a portion of the compound hybridises with RNA coff companies which is a setholycytosine. The antisense compound may comparise an antisense modely, or nucleobase. It has at least one cytosine which is a 5-methylcytosine. The antisense compound may comparise an antisense mucleic acid molecule that is specifically whybridisable with a 5'-untranslated region (UTR), with a start region, with a 3'-UTR, with an intron-cevon junction of a nucleic acid molecule encoding kinesin-like 1. ISIS #344902.
                                                                                      New antisense compound 8 to 80 nucleobases in length targeted to a nucleic acid molecule encoding kinesin-like 1, useful for treating an animal having a disease or condition such as cancer, tumor, autoimmune
                                                                                                                                                                                                               Example 30; SEQ ID NO 129; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinesin-like 1, ISIS #344902
Koller E;
                                                WPI; 2004-652550/63
Dobie KW,
                                                                                                                                                                    disease.
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Gaps ö 62.0%; Score 12.4; DB 13; Length 20; 92.9%; Pred. No. 3.3e+04; tive 0; Mismatches 1; Indels 0 Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other; Best Local Similarity 92.8 Matches 13; Conservative Query Match

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ADR72397 standard; DNA; 20 ADR72397; ADR72397/

BP.

Antisense oligo targeted to mouse kinesin-like 1, ISIS 285690.

02-DEC-2004 (first entry)

Antisense; kinesin-like 1; N2 kinesin; bimC kinesin; cellular proliferation; cancer; B-cell leukaemia; autoimmune disease; carpal tunnel byrdrome; Rayraud's phenomenon; systemic sclerosis; Sjorgren's syndrome; rheumatoid arthritis; polymyositis; polyarteritis; systemic lupus erythematosus; mouse; ss; human.

Homo sapiens. Synthetic. Mus musculus.

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The present invention relates to antisense compounds, compositions and methods for modulating the expression of kinesin-like 1. The superfamily of kinesins function as molecular engines to bind and transport vesicles and organelles along microtubules using energy supplied by ATP. Kinesin-like 1, a member of the N2 (also called bind) family of kinesin, is involved in separating the chromosomes by directing their movement along microtubules in the bipolar spindle. Kinesin-like 1 is also known as KNSII, Egs, HRSP, KIFII, thyroid interacting protein 5 and TRIPS. Inhibition of kinesin-like 1 may be a target for arresting cellular of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, autoimmune diseases such as carpal tunnel syndrome, of kinesin-like 1 expression may contribute to other disease states such as B-cell leukaemia, uncience slerosis, Sjorgare's syndrome, rheumatoid arthritis, polymyositis and polyarteritis. Kinesin-like 1 is an autoantigen identified in systemic lupus erythematosus. The invention contributes to antisense uncieic acid oligomers, targeted to the gene concoding kinesin-like 1. Also provided are methods of screening for modulators of kinesin-like 1. Also provided are methods of screening for confine cytosine which is a 5-methylocytosine. The antisense compound may comprise an antisense mucleic acid molecule that is specifically hybridisable with a 5'-untranslated region (UTR), with a start region, with a 3'-UTR, with an intron-confine second molecule encoding kinesin-like 1 expensed molecule encoding expense to modelice acid molecule encoding kinesin-like 1 expense synthesised via solid phase P(III) phosphoramidite confine confine confine confin
                                                                                      /note= "OTHER= phosphorothioate nucleotide. All cytosines are 5-methylcytidines. Residues 1 to 5 and 15 to 20 are 2'-methoxyethyl nucleotides."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compound 8 to 80 nucleobases in length targeted to a nucleic acid molecule encoding kinesin-like 1, useful for treating an animal having a disease or condition such as cancer, tumor, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 36; SEQ ID NO 161; 110pp; English.
Location/Qualifiers
                                                                       /mod base= OTHER
                                                                                                                                                                                                                                                                                 17-NOV-2003; 2003US-00714796
                                                                                                                                                                                                                                                                                                                                   23-MAY-2002; 2002US-00156603
                             1. .20
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dobie KW, Koller E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-652550/63.
                                                                                                                                                                                                                                                                                                                                                                                  (DOBI/) DOBIE K W.
                                                                                                                                                                                                                                                                                                                                                                                                          (KOLL/) KOLLER E.
                                                                                                                                                                                           US2004180847-A1.
    Key
modified_base
                                                                                                                                                                                                                                          16-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease.
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Score 12.4; DB 13; Length 20; Pred. No. 3.3e+04; 0; Mismatches 1; Indels 62.0%; TCTTGCAGGAAGCG 17 13; Conservative Local Similarity Query Match Matches

19 TCTTGCAGGAAGTG 6

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Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

kinesin-like 1.

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Gaps

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RESULT 21

Length 17;

61.0%;

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The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.
                                                                                                                                                                                                    Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.
                                                                                                                                                             Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shannon ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
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                     ABN08122 standard; DNA; 17 BP
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30-JAN-2001; 2001WO-US000669.
30-JAN-2001; 2001WO-US000670.
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30-JAN-2001, 2001WO-US000662.
30-JAN-2001, 2001WO-US000663.
30-JAN-2001, 2001WO-US000664.
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30-JAN-2001; 2001WO-US000666
30-JAN-2001; 2001WO-US000667
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2000US-0236359P.
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                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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ABN08122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel myosin-like protein-1, useful for treating or preventing disorder associated with decreased expression or activity of human genome-derived myosin-like protein-1 such as disorder of heart and/or skeletal muscle
                                                                                                                                                                                                                                                                                                                                                        Human; ss; probe; myosin-like protein-l; hGDMLP-l; hGDMLP-l agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder; skeletal muscle function.
                                        Gaps
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                                        3; Indels
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Score 12.2; DB 6;
Pred. No. 4.1e+04;
0; Mismatches 3;
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
2001WO-US000661.
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2001US-00866108
                       82.48;
                                                                           4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                            ACN71212 standard; DNA; 17
                                                                                                                                                                                                                                                                                     02-DEC-2004 (first entry)
 Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ji Y, Penn SG,
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HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANK D.
CHEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004137589-A1.
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30-JAN-2001;
30-JAN-2001;
30-JAN-2001;
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30-JAN-2001;
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(JIYY/)
(PENN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEN/)
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(RANK/
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                                                                                                                                                                         RESULT 22
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08-JUN-2000
                                               AAA83794;
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                                                                                                                                          Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                   Tritz R,
  RESULT 24
             AAA83794/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a novel method for determining the risk of or diagnosing Alzheimer's disease using single nucleotide polymorphisms (SNPs) present in an individual's mitochondrial DNA (mtDNA). In additon, the SNPs identified can be used to identify agents suitable for use in treating Alzheimer's disease. Sequences AAC67301-C67610 are PCR primers used to demonstrate the method of the invention
antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A pharmaceutical composition of the invention is useful for treating or preventing a disorder associated with decreased expression or activity hGDMLP-1, such as a disorder of heart and/or skeletal muscle function. The present sequence represents a 17-mer nucleotide, used in the
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing a subject at the risk for or having Alzheimer's disease comprises determining at least one single nucleotide polymorphism in mitochondrial DNA associated with the disease in the sample from the
                                                                                                                                                                                                                                                                                                                                Human; mitochondrial genome; single nucleotide polymorphism; SNP;
Alzheimer's disease; mtDNA; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                          Alzheimer's disease-linked mitochondrial SNP PCR primer #155.
                                                                                                        Score 12.2; DB 13; Length 17; Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.2; DB 3; Length 18; Pred. No. 4.1e+04; 0; Mismatches 3; Indels
                                                           invention for scanning the sequence represented in ACN63103
                                                                                                                                 Indels
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                                                                                  Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
                                                                                                                                 0; Mismatches
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                                                                                                        61.0%;
llarity 82.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                  TCCTGCCAGAAGCGGCT
                                                                                                                                                     4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                                                      AAC67455 standard; DNA; 18
                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                  Local Similarity
nes 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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22-OCT-1999;
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                                                                                                                                                                                                                                                              AAC67455;
                                                                                                          Query Match
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                                                                                                                     Best Loc
Matches
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17 ATTCTTGCACGAAACGG 1

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ACTUTTGCAGGAAGCGG

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                                                                                                                                                                                                   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to a hairpin or hammerhead ribozyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAAB2415 to AAAB6787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient
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Pred. No. 4.1e+04;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robbins JM;
                                                                                                                                                    cdk-we-hu ribozyme binding site #269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 67; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Welch PJ, Barber JR,
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AAA83794 standard; DNA; 19
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                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restenosis treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-412314/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                      WO200032765-A2.
                                                                                                   04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998;
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Vogelstein

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This invention relates to a novel activated mutant protein tyrosine kinases and associated methods for diagnosing cancer and screening for anti-cancer agents. Protein kinases are signalling molecules involved in tumourigenesis. Mutational analysis of the human tyrosine kinase gene family identified somatic alteration sin 1 in 5 colorectal cancers, with the majority of mutations occurring in the NTRK3, FES, GUCY2F and MCCK/MIK4 genes. Most were identified in the kinase domain. The invention may be useful for the production of compounds with a cytostatic activity acting as protein tyrosine kinase inhibitors or guanylate cyclase stimulators. The invention may be useful for developing methods for
                                                                                                                                                                                                                                                                                                                                        Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and associated methods for diagnosing cancer and screening for anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting mutations involved in cancer or screening for anti-cancer agents. The present sequence is that of a human-derived oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maspin; serpin; mammary epithelial cell; human; promoter; malignant; tumour cell; treatment; prostate cancer; breast cancer; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.0%; Score 12.2; DB 13; Length 19; 82.4%; Pred. No. 4.1e+04; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human maspin Ets wild-type sense oligonucleotide DNA.
                                                                                                                                                                                                                                                    Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 6 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 1786; 363pp; English
                                                                                                                                                                                                                                                       Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DAND ) DANA FARBER CANCER INST. (PARD/) PARDEE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT89003 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACTCTTGCAGGAAGCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US005186.
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                                                                                        18-FEB-2004; 2004WO-US004452.
                                                                                                                                      21-FEB-2003; 2003US-0448537P.
29-MAY-2003; 2003US-0473895P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTGCTGCAGGAACG
                                                                                                                                                                                                         SNIXAOH SUHOC VINU ( OCYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                         Parsons W,
                                                                                                                                                                                                                                                                                                    WPI; 2004-718702/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
WO2004082458-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9736179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-1997.
                                                                                                                                                                                                                                                         Bardelli A,
                                           30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT89003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                             agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme [1] which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule [11] comprising a promoter operably linked to a nucleic acid segment encoding [1]. [1] can have antipsoriatic, christopatic, antiseborrheic, antidiabetic, antisickling, ophthalmological, cytostatic, antiseborrheic, antidiabetic, antisickling, chartanological, vulnerary, keratolytic and virucide activities, and cleaves RNA encoding cytokine involved in inflammation. [1] can be used in gene therapy. [1] and [11] are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, aquamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detechment, and for treating and preventing carring such as keloid, adhesion and hypertrophic or hypertrophic burn sear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
GUCY2F; MCCK; MLK4; Kinase domain; cytostatic; tyrosine kinase inhibitor;
guanylate cyclase stimulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel mutant protein tyrosine kinase-related oligonucleotide SeqID1786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 5 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.2; DB 5;
Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 172; 408pp; English.
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82.4%;
                                                                                                                                                                                                           26-OCT-2000; 2000WO-US029500
sickle cell retinopathy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ACTOTTTCTAGAAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT01798 standard; DNA; 19
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nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                  Robbins JM, Tritz R;
                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUSOL INC.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-300427/31.
                                                                                                                WO200130362-A2
                                             Homo sapiens
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                                                                                                                                                                03-MAY-2001
                                                                       Synthetic
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Matches

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Gaps

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Matches
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AAX79782/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; gential disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                               experiments to analyse the maspin promoter region. AATP9003 is designed as a Ets regulatory element wild type (WT) sense oligonucleotide. Maspin is a scrpin which is expressed in mammary epithelial cells. Its expression in these cells decreases with increasing malignancy and is lost in during metastasis. Maspin protein is also known to inhibit the mobility of tumour cells. This gene can be used in method for screening compounds to identify candidate compounds for the treatment of prostate cancer. It can also be used to identify compounds that increase the expression of maspin, and for detecting the presence of metastatic prostate epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primers AAZ01426-Z06209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
                                              Maspin gene promoter fragment - used to identify compounds for treatment of prostate or breast cancer.
                                                                                                        Primers AAT89003-T89008 are used in electrophoretic mobility shift assay
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                         Score 12.2; DB 2; Length 20;
Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                      Sequence 20 BP; 3 A; 11 C; 3 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1492; 1755pp; English.
                                                                                   Disclosure; Page 12; 51pp; English
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                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                      20
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97FR-00016034.
98US-0107077P.
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                                                                                                                                                                                                                                                          / Match 61.0%;
Local Similarity 82.4%;
les 14; Conservative
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                                                                                                                                                                                                                                                                                                     4 TCTTGCAGGAAGCGGCT
                                                                                                                                                                                                                                                                                                                                                                              AAZ02042 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31
                               WPI; 1997-489785/45
            Zhang M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1998;
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04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                  AAZ02042;
            Sagar R,
                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                       Best Loca
Matches
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                        against Chlamydia trachomatis. Antiennes and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, allpingitis, perimpatitis, bartholinitis; penumopathy in breast feeding infants; and venezeal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these
polypeptides (see AAY36754-Y37949) which can be used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic diagnosis using human mitochondrial DNA - comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer; human; mitochondrial DNA; genetic diagnosis; adult disease contraction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.0%; Score 12.2; DB 2;
82.4%; Pred. No. 4.1e+04;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer H15340 for mitochondrial DNA analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                      2; DB 2;
4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                      61.0%; Score 12.2; D
82.4%; Pred. No. 4.1e
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GACTCTTGCAGGAAGCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97JP-00279127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX79782 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-320841/27
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          base replacements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANA/) TANAKA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP11113597-A.
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2 ACTCTTGCAGGAAGCGG 18

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Gierse JK;
                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                  Gene detection method using human mitochondrial DNA to reveal and confirm amino acid substitution advantageous or disadvantageous in prolonged survival of human, useful for diagnosis of Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a detection method using human mitochondrial (mt) DNA. The method comprises detecting the replacement of a base accompanying an amino acid substitution in a protein encoded by its base sequence in a human mitochondrial DNA base sequence. The method is useful for diagnosis of Parkinson's disease, and in health checks and assessing risks for other adult diseases. The present sequence is a PCR primer, which was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nostropic; antiarthritic; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation;
                                                                                                                                                             Human; mitochondrial; Parkinson's disease; cytochrome b; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%; Score 12.2; DB 8; Length 20; 82.4%; Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 20 BP; 5 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                 (GIFU-) GIFU INT INST BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 35pp; Japanese.
                                                                                                                                     Human cytochrome b PCR primer #10
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ATTCTTGCACGAAACGG
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ACC70917 standard; DNA; 20
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                                                                                                                                                                                    Homo sapiens
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                                                                                                                 20-NOV-2003
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Matches
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The present sequence represents a chimeric antisense oligonucleotide targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The human megras-1 gene is located on chromosome 9, more specifically to human megras-1 gene is located on chromosome 9, more specifically to or graving a sequence comprising 8-30 bp targeted to a nucleic acid encoding megras-1, which specifically hybridise with the nucleic acid encoding inhibits its expression; (2) a method of inhibiting the expression of inhibits its expression; (2) a method of inhibiting the expression of mPGES-1 in cells or tissues; and (3) a method of treating an animal condition associated with megras-1. MPGES-1 chimeric articlabetic, immunomodulator, cardiant, neuroprotective, antiathritic, vasotropic, antidiametricy, neuroprotective, nootropic, antiathritics, and can composition of phthalmological, immunomodulatory and cardiovascular activities, and can be used as mPGES-1 inhibitors and in gene therapy. The antisense compound to be used as mPGES-1 inhibitors and in gene therapy. The antisense compound can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or condition associated with mPGES-1 e.g., inflammation injury, or condition immunological, cardiovascular or neurological disorder.
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/note= "phosphorothioate linkages and all cytidine
residues are 5-methylcytidines"
Alzheimer's disease, arthritis, diabetes, cancer, ischaemia, reperfusion injury, ophthalmic disorder, immunological disorder; cardiovascular disorder, neurological disorder; ss.
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Pred. No. 4.1e+04;
0; Mismatches 3;
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/note= "2'-0-methocyethyls"
16. .20
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/note= "2'-O-methoxyethyls"
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                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                     Key
modified_base
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                                                                                                                chimeric; antisense oligonucleotide; phosphorothioate; human; microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor; microsomal prostaglandin E2 synthase; hmPGES-1; mPGES-1 inhibitor; inmuclator; cardiant; E synthase; inhibitor; cytostatic; antidiabetic; immunomodulator; cardiant; neuroprotective; antiinflammatory; neuroprotective; nationflammatory; neuroprotective; vasotropic; ophthalmological; immunomodulatory; cardiovascular; gene therapy; inflammation; Alzheimer's disease; arthritis; diabetes; cancer; ischaemia; reperfusion injury; ophthalmic disorder; immunological disorder; cardiovascular disorder; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compound, having a sequence targeted to a nucleic acid encoding mPGES-1, useful for preparing a composition for treating e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
                                                                                                                                                                                                                                                                                                           /mod_base= OTHER/nothioate linkages and all cytidine residues are 5-methylcytidines"
                                                                                            Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:692.
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/note= "2'-O-methoxyethyls"
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/note= "2'-0-methocyethyls"
16. .20
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                        BP.
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                         ADM14505 standard; DNA; 20
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                                                                                                                                                                                                                                                     Synthetic.
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                                                 ADM14505;
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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for Insulin-like Growth Factor [IGRF]-1 receptor, IGF binding protein [IGRB]-2 or IGRBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, conformation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-0190nucleotides of the present invention (see AAF45151 and AAF45153-0160nucleotides of the present invention of the skin, a neoplasias, scleroderma, warfs, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid; skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis; IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neovascular condition of the retina; ss.
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can be used for preparing a composition for treating a disease or condition associated with mPGES-1 e.g., inflammation, Alzheimer's disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, ophthalmic, immunological, cardiovascular or neurological disorder.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                              61.0%; Score 12.2; DB 12;
82.4%; Pred. No. 4.1e+04;
ive 0; Mismatches 3;
                                                                                                                                                                                                    Seguence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                  Local Similarity 82.4
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                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                    datches
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100.0%; Pred. No. 5.1e+04;

Best Local Similarity

18

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The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense eoligonucleotide, (for Insulin-like Growth Factor [IGF9-1] receptor, IGF binding protein [IGF89-2 or IGF893), which is capable of inhibiting or reducing growth factor mediated cell proliferation, if Imflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the antisense oligonucleotide which can be used to design the effects of psoriasis, colligonucleotides of the present invention (see AAP45151 and AAP45153-1845161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborthoea, keloids, keratosis, colligonucleotides of the skin, a hyperneovascular condition as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic; cytostatic; dermatological; cardiant; virucide; ophthalmological; Keloid; skin disorder; Insulin-like Growth Factor I receptor; IGF-1; pityriasis; IGF binding protein; IGFB-2; IGFBB3; inflammation; psoriasis; pilatis; growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba; Keatosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease; hyperneovascular condition; hyperplasia; kidney disease; neobascular condition; hyperplasia; kidney disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or
                                                                                                   Gaps
                                                                                                ;
                                                           Length 15;
                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
                  Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
                                                      60.0%; Score 12; DB 4; Le
100.0%; Pred. No. 5.1e+04;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edmondson SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MURD-) MURDOCH CHILDRENS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 44; 201pp; English.
                                                                                                                                                                                                                                                                                      ВР.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2000; 2000WO-AU000693
                                                                                                                                                                                                                                                                                    AAF46588 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            IGFBP3 oligonucleotide #8.
                                                                         Local Similarity 100.
nes 12; Conservative
                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wraight CJ, Werther GA,
                                                                                                                                                                               12 gcaggaagcggc 1
                                                                                                                                         8 GCAGGAAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000,
                                                                                                                                                                                                                                                                                                                            AAF46588;
                                                           Query Match
                                                                                                Matches
                                                                                                                                                                                                                                                                 AAF46588/
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60.0%; Score 12; DB 4; Length 15;

Query Match

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The invention relates to a novel isolated 17 mer nucleic acid sequence, and in the specification, a sequence containing at least 15 consecutive connected sequence, as sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of angles for them, or the corresponding RNA. The novel isolated nucleic coid of any of them, or the corresponding RNA. The novel; solated nucleic coid acids of the invention are useful as probes and primers for detecting, identifying and/or amplifying a nucleic acid, e.g. as one component of a gene chip, in vitro as (anti) sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, concentration of recombinant polypeptides. Any of the nucleic acids, concentration of parameterized against the polypeptides are useful for vector or antibodies directed against the polypeptides are useful for desense that are characterised by development of tumours or call desensation, specifically cancer but also Alzheimer's disease and correspondence of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these companies. The polypeptides can also be used to generate antibodies, and chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression correlated human fukutin oligonucleotide of the invention
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ö
                                                                                                                                                                                                                                                                                                                                                              Cytostatic, virucide, neuroprotective, nootropic, neuroleptic, gene chip, antisense, sense, tumour, cell degeneration, cancer, Alzheimer's disease, schizophrenia, protein chip, gene therapy, tumour suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid, useful for treating viral diseases associated with tumors and cell degeneration, also related polypeptides, antibodies and transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  Gaps
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                                                                                                                                                                                                                                                                                                                       Tumour suppression related human fukutin oligo SEQ ID No 397.
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Indels
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Mismatches
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                                                                                                                                                                                             ABT34760 standard; DNA; 17 BP.
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                                                                                                                                                                                                                                                                               12-JUN-2003 (first entry)
  12; Conservative
                                            20
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                                                                                   15 CAGGAAGCGGCT
                                            9 CAGGAAGCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 human fukutin; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                       ABT34760;
Matches
                                                                                                                                                   RESULT 35
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21-APR-1998;
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        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 38
8
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                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences associated with tumor suppression, regression, apoptosis or virus resistance are useful to diagnose and treat viral disease, development of tumor cells and cell degeneration.
                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents an isolated nucleic acid sequence associated with tumour suppression or regression, apoptosis or virus resistance. invention relates to these sequences or sequences having at least 80% identity to them, and polypeptides encoded by the sequences or polypeptides having 80% identity to the polypeptide sequences. The invention is used to diagnose or treat viral disease or disease characterized by development of tumour cells or cellular degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; single nucleotide polymorphism; microarray; side effect; ss; primer; PCR.
                                                                                                                                                ss; tumour suppressor; antitumour; cytostatic; tumour suppression; tumour regression; apoptosis; virus resistance; diagnosis; cellular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single nucleotide polymorphism detection primer, SEQ ID No 1567.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 17 BP; 5 A; 2 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                              Human tumour suppressor seguence #3140.
                                                                                                                                                                                                                                                                                                  Amson R;
                                                                                                                                                                                                                                                                                SA.
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 765; 798pp; French.
                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR ENGINES LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF87984 standard; DNA; 19 BP.
                                                                       ACC54373 standard; DNA; 17 BP.
                                                                                                                                                                                                                                            20-JUN-2001; 2001FR-00008139
                                                                                                                                                                                                                                                              20-JUN-2001; 2001FR-00008139
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                   Telerman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TCTTGCAGGAAG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTGCAGGAAG 14
         13
         2 ACTCTTGCAGGA
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                                                                                                                                                                                      Homo sapiens
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                                                                                                            27-JUN-2003
                                                                                                                                                                                                                                                                                                   Tuijnder M,
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Matches
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The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA crayments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing oligo. The isolated human cameroarray equipped with the SNP containing oligo. The isolated human collaboration is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents one of the PCR primers used in the single nucleotide polymorphism cone of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide useful for detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human biallelic marker downstream amplification primer SEQ ID NO:8500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 1 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 1567; 704pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ74144 standard; DNA; 20 BP.
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                                                                                                                                                                                                               12-FEB-2002; 2002JP-00034717.
                                                                                                                                                                                                                                                                                        12-FEB-2002; 2002JP-00034717.
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nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 CAGGAAGCGGCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-820454/77
                                                                 JP2003235571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in human gene
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Zwick M, Pavco P,
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                                                       WPI; 2002-049286/06
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Best Local Similarity
                Mathies RA;
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                  Κu Ή,
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                                                                                                                                                                                                                                                    AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from differential efficacious responses to and side effects from M.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3056, 3157, 327, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the
                                                                                                                                                          Novel biallelic markers used to construct a high density disequilibrium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-nucleotide polymorphism, SNP, diabetes; thalassaemia; sickle-cell ansemia; cystic fibrosis; oncogenic mutation; pathogen; paternity; prematal testing; forensic investigation; genotyping; of second of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.0%; Score 12; DB 3; Length 20; 75.0%; Pred. No. 5.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein lipase precursor SNP-5 reverse PCR primer.
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/mod base= OTHER
/note= "6-carboxy-x-rhodamine (ROX)"
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                                                                              Chumakov I;
                                                                                                                                                                                                                     Claim 8; Page 2043; 2745pp; English.
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98US-0109732P
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                                                                              Blumenfeld M,
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                                                                                                                     WPI; 2000-013267/01
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Matches 15; Conserv
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  23-NOV-1998;
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                                                                                Cohen D,
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The present sequence is that of a labelled PCR primer used to amplify and genotype the partial nucleotide sequence of lipoprotein lipase precursor (LPD.) surrounding the single-nucleotide polymorphism (SNP) - S site given in ABA02531. The specification describes a novel method for analysing a cortiant site (VS) in a target nucleotides a novel method for analysing a cortiant site (VS) in a target nucleotides a lower maplified sequence specifically by extending two primers (Pl. P2) in the presence of a colymerase having 3'-5'-exonuclease activity. Pl is labelled on at least one nucleotide (nt) other than the 3'-terminal nt and it anneals to a region that spans VS in the first strand of NA. P2 is complementary to cregion in the complementary second strand of NA. If pl is complementary to to the base occupying VS it will be extended to form a labelled product. If Pl is not complementary the polymerase will digest Pl from its 3'-end, cremoving the label, and any extension product will be unlabelled. The extension products are analysed for absence/presence of the label. The method of the invention is particularly used to detect point mutations or product of the invention is particularly used to detect point mutations sickle-cell anaemia, cystic fibrosis or oncogenic mutations, or for assessing predisposition to these conditions or monitoring the effect of treatments. Other applications are detecting pathogens (including those treatments and in prenatal testing or forensic investigations. The method can be used for simultaneous analysis of many different VS, in one or more targets, providing very high throughput and rapid genotyping
Analyzing variant sites in nucleic acid, useful e.g. for detecting disease-associated polymorphisms, comprises extension of labeled primer in presence of polymerase with 3'-5'-exonuclease activity.
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Mcswiggen J;

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The present invention relates to enzymatic and antisense nucleic acid molecules that act as inhibitors of the expression of repressor genes encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription factor gene, IRF-2 and/or the CAATT Displacement Protein (CDP). Inhibition of the repressors removes prevents inhibition (and consequently increases expression of) genes involved in the production of erythropoietin, granulocyte colony stimulating factor protein and interferon alpha
                                       Enzymatic and antisense nucleic acid inhibition of repressor genes, useful for producing e.g. granulocyte colony stimulating factor protein, interferon alpha and erythropoietin.
                                                                                                                                     Claim 54; Page 134; 164pp; English.
WPI; 2000-647423/62.
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ö 59.0%; Score 11.8; DB 3; Length 17; 86.7%; Pred. No. 6.4e+04; Live 0; Mismatches 2; Indels 1 GACTCTTGCAGGAAG 15 1 GACTATTTCAGGAAG 15 Query Match
Best Local Similarity 86.7
Matches 13, Conservative ð 셤

Sequence 17 BP; 6 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

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Sequence 319, App
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Sequence 814, App
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Sequence 507, App
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10. US-10-339-674-1348
10. US-10-339-674-1348
10. US-10-339-674-1348
10. US-10-398-138-134
10. US-10-984-198-134
10. US-10-987-092-134
10. US-10-984-199-135-1013
20. US-10-984-919-1512
20. US-10-998-226
20. US-10-91-919-919-1512
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20. US-10-923-522-70
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US-09-866-108-117
US-09-866-108-118
US-09-866-108-6215
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/ cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

/ cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

/ cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

/ cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

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US-10-773-678-343
US-10-773-678-344
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                                                                                                                                              August
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US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Attisense Oligonucleotide Modulation of STAT3;
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Expression
; FILE REPERENCE: ISPH-0828
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: US/10/713,678
; PRIOR PILING DATE: 2001-01-11
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-04-06
; PRIOR FILING DATE: 2000-04-06
; RIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; NUMBER OF SEQ ID NOS: 422
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Publication No. US20050074879A1
GENERAL INFORMATION:
APPLICANT: Karras, James G
TILLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
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Pred. No. 6.5;
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95.0%; Score 19; DB 21;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0;
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PRIOR APPLICATION UNMBER: 10/713,139
PRIOR FILING DATE: 2004-02-06
PRIOR FILING DATE: 2003-11-14
PRIOR PELING DATE: 2003-11-14
PRIOR PELING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-04-06
SOUTHARE: PELING DATE: 1999-04-08
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LENGTH: 20
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                                                                                          116, App
117, App
119, App
6215, Ap
6217, Ap
6217, Ap
6218, Ap
6218, Ap
19, App
19, Ap
                                                                                                                 Sequence 117,
Sequence 118,
Sequence 6215,
Sequence 6215,
Sequence 6216,
Sequence 6217,
Sequence 6218,
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Sequence 342, Application US/10773678

Publication No. US2005007487941

Sequence 100. US2005007487941

Septence 100. US2005007487941

SEPTENCE INFORMATION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Expression
FILE REFERENCE: ISSH-0828

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT PELING DATE: 2004-02-06

PRIOR PILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-01-14

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 342
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Sequence
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US-10-773-678-179
Sequence 179, Application US/10773678
Publication No. US20050074879A1
GENERAL INFORMATION:
TITLE OF INVENTION: Antiense Gligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
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                             US-10-060-830-125

US-10-723-361-115

US-10-723-361-116

US-10-723-361-118

US-10-723-361-119

US-10-723-361-6215

US-10-723-361-6216

US-10-723-361-6216

US-10-723-361-6219

US-10-723-762-6247

US-10-316-516-76
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; Sequence 339, Application US/10773678
; Publication No. US20050074879A1
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US-10-857-715-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GACTCTTGCAGGAAGCG 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-773-678-339
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Sequence 340, Application US/10773678

Publication No. US20050074879A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Karras, James G

TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0828

CURRENT APPLICATION NUMBER: US/10/773,678

CURRENT PILING DATE: 2004-02-06

PRIOR APPLICATION NUMBER: 10/713,139

PRIOR APPLICATION NUMBER: 09/758,881

PRIOR APPLICATION NUMBER: 09/758,881

PRIOR APPLICATION NUMBER: 09/758,461

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 402

SEQ ID NO 340

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%; Score 18; DB 21; Length 20; 100.0%; Pred. No. 22; tive 0; Mismatches 0; Indels
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, OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-340
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FILE OF INVENTION: Expression
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: Patentin Ver. 2.1
LENGTH: 20
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Best Local Similarity 100.0
Matches 18; Conservative
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US-10-773-678-340
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ATTLE OF INVENTION: Antisense Oligonuclectide Modulation of STAT3
TITLE OF INVENTION: Antisense Oligonuclectide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: 02/10/773,678
CURRENT PILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR APPLICATION NUMBER: POT/95,881
PRIOR FILING DATE: 2003-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: Patentin Ver. 2.1
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Sequence 201, Application US/10857715

Sequence 201, Application US/10857715

Sequence 201, Application Wo. US20050164218A1

GENERAL INFORMATION:

APPLICANT: Barks Joint

APPLICANT: Bark Steven

TITLE OF INVENTION: Gene Expression Markers for Response to TITLE OP INVENTION: Gene Expression Markers for Response to TITLE OP INVENTION: Gene Expression Markers for Response to TITLE OP INVENTION: Gene Expression Markers for Response to TITLE OP INVENTION: UNMBER: US/10/857,715

CURRENT APPLICATION NUMBER: 00/474,908

FRIOR FILING DATE: 2003-05-30

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 201

LENGTH: 20
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80.0%; Score 16; DB 22; L
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0;
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; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344
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Best Local Similarity 100.0%; Pred. No. 73;
Matches 17; Conservative 0; Mismatches
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TITLE OF INVENTION: Antisense Oligonuclectide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0029
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: 10/713,139
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 09/758,881
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR PILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 402
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 345
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Antisense oligonucleotide US-10-773-678-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-10-773-678-345
; Sequence 345, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15, Conservative
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Sequence 19, Application US/09758881

Sequence 19, Application US/09758881

Patent No. US2001029250A1

GENERAL INFORMATION:

APPLICATON: Marisease G

TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0532

CURRENT APPLICATION NUMBER: US/09/758,881

CURRENT FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR APPLICATION NUMBER: PCT/US00/09054

PRIOR APPLICATION NUMBER: 1999-04-08

NUMBER: OF SEQ ID NOS: 152

SEQ ID NO 19

SEQ ID NO 19

LENGTH: 20
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TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
TITLE OF INVENTION: Expression
FILE OF INVENTION: Expression
FILE REPERENCE: ISPH-0828
CURRENT APPLICATION NUMBER: US/10/773,678
CURRENT PILING DATE: 2004-02-06
PRIOR PILING DATE: 2003-11-14
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 099-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
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Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0;
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; Publication No. US20050074879A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 20
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US-10-773-678-19
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RESULT 12 US-10-671-395-1012/c

RESULT 10

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1778
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                                                                                                                                         = negative ConnectronObjectNumber =
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OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber US-10-339-674-1348
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; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber
US-10-339-674-1349
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; Sequence 1349, Application US/10339674
; GENERAL INFORMATION:
; APPLICARY: Feldmann, Richard J.; Global Determinants, Inc.
; TILLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.;
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT PILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1348, Application US/10339674
Publication No. US20030204318A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PELING NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3537
SOFTWARE: Proprietary
SEQ ID NO 1348
LENGTH: 19
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64.0%; Score 12.8; DB 17; Length 19;

Best Local Similarity 87.5%; Pred. No. 1.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels
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ORGANISM: Escherichia coli K-12 MG1655 complete genome.
                       LENGTH: 18
TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655 complete genome.
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Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2;
                                                                                               ; FEATURE:
; LOCATION: (1734068)...(1734085)
; OTHER INFORMATION: Chromosome = 1 Strand
18-10-339-674-1351
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Best Local Similarity 87.5%; Pr
Matches 14; Conservative 0;
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US-10-339-674-1349
SEQ ID NO 1351
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            Deblication No. US20040132063Al
GENERAL INFORMATION:
APPLICANT: Pharmacia Corp.
APPLICANT: Pharmacia Corp.
APPLICANT: Pharmacia Corp.
APPLICANT: Gerse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
PRIOR PILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SSFTWARE: Patentin version 3.2
LENGTH: 20
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Chromosome = 1 Strand = positive ConnectronObjectNumber US-10-339-674-1350
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Sublication No. US20030204318A1

GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT PILING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 3537
SOFTWARE: Proprietary
SEQ ID NO 1350
LENGTH: 17
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TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/339,674
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 3337
SOFTWARE: Proprietary
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Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismaran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%; Score 13.6; DB 19;
80.0%; Pred. No. 4.4e+03;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Human PGE2 antisense
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  Sequence 1012, Application US/10671395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GACTCTTGCAGGAAGCGGCT 20
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                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: artificial
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US-10-339-674-1350/c
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US-10-339-674-1351
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Factors Altering Tumor Necrosis
Factor Receptor Releasing Enzyme Activity, and Methods
of Use Thereof
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                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,198
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/10793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22000-20577.21
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/081,385
FILING DATE: 09/081,385
FILING DATE: 09/081,385
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 06/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WM. Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20
TELEPHONE: 650-813-5600
TELEPHONE: 650-813-5600
             TITLE OF INVENTION: Factors Alterin
TITLE OF INVENTION: Factor Receptor
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 14; Conserval
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US-10-967-092-134
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                                                                                                                                                                                                                            Sequence 134, Application US/09752639
Patent No. US20020091243A1
GENERAL INFORMATION:
APPLICANT: Gatanger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: Of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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64.0%; Score 12.8; DB 9;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows
SOFTWARE: FRAESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,639
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: PCT/US99/10793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELEPHONE: 650-813-5600
TELEPHONE: 650-494-0792
TELEPHONE: 650-494-0792
TELERA: 706141
INFORMATION FOR SEQ ID NO: 134: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLACTORY
FILING DATE:
APPLICATION NUMBER: 09/081,385
FILING DATE:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WW, FEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304-1018 FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPATIBLE COMPATIBLE COMPATIBLE COMPATIBLE COMPUTER: IBM COMPATIBLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 134, Application US/09984198
Patent No. US20020106679A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
APPLICANT: Granger, G.A.
                       TCTTGCAGGAAGCGGC 19
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Sequence 571, Application US/10671395
; Sequence 571, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
    APPLICANT: Pharmacia Corp.
; APPLICANT: Paramacia Corp.
; APPLICANT: Gierse, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT PILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/413,549
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 571
LENGTH: 20
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Pred. No. 1.5e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                 REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEPFAX: 650-494-0792
           FILING DATE: 13-Nov-2000
APPLICATION NUMBER: US/09/081,385
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-11-011-500-134
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                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 134:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 78.>
Local Similarity 78.>
Local Similarity 78.>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-671-395-1013/c
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Publication No. US20050158826A1
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
Granger, G.A.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
of Use Thereof
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ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBW Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION DATE: US/11/011,500
FILING DATE: 13-Dec-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/10/967,092
FILING DATE: 15-Oct-2004
                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 64.0%; Score 12.8; DB 21;
Best Local Similarity 87.5%; Pred. No. 1.1e+04;
Matches 14; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 41,386
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/712,813
FILING DATE: 13-Nov-2000
APPLICATION NUMBER: US/09/081,385
FILING DATE: 4Uhknown>
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: WU, Frank
                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/967,092
FILING DATE: 15-Oct-2004
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 134: US-10-967-092-134
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO: 134:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING KCNEI AS AN LQT GENE
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Pred. No. 1.9e+04;
0; Mismatches 1; Indels
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APPLICANT: Sanguinetti, Michael C.
APPLICANT: Curran, Mark E.
APPLICANT: Curran, Mark E.
APPLICANT: Curades, Gregory M.
APPLICANT: Connors, Timothy D.
APPLICANT: Splawski, 190.
APPLICANT: Splawski, 190.
TITLE OF INVENTION: KVLQTI - A LONG QT SYNDROME GENE TITLE OF INVENTION: KVLQTI - A LONG QT SYNDROME GENE FILE REFERENCE: 2323-163
CURRENT APPLICATION NUMBER: US 09/597,731
PRIOR APPLICATION NUMBER: US 09/597,731
PRIOR APPLICATION NUMBER: US 09/135,010
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR FILING DATE: 1999-08-29
PRIOR FILING DATE: 1999-08-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-10-29
PRIOR APPLICATION NUMBER: US 60/019,014
PRIOR PILING DATE: 1995-10-29
PRIOR FILING DATE: 1995-11-2-22
PRIOR APPLICATION NUMBER: US 60/019,014
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Pred. No. 1.9e+04;
0; Mismatches 1;
TITLE OF INVENTION: CAUSE ARRYTHMIA SUSCEPT TITLE OF INVENTION: KCNE1 AS AN LQT GENE FILE REFERENCE: 2323-162
CURRENT APPLICATION NUMBER: US/10/138,316
CURRENT FILING DATE: 2002-05-06
PRIOR PLING DATE: 1999-11-22
PRIOR PLING DATE: 1999-08-17
PRIOR FLING DATE: 1999-08-17
PRIOR FLING DATE: 1999-08-17
PRIOR FLING DATE: 1999-08-17
PRIOR FLING DATE: 1997-08-29
PRIOR FILING DATE: 1996-08-17
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1996-09-17
PRIOR FILING DATE: 1996-10-29
PRIOR PLING DATE: 1996-10-29
PRIOR PLING DATE: 1996-10-29
PRIOR PLING DATE: 1996-12-22
PRIOR PLING DATE: 1996-10-29
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Publication No. US20030170708A1
GENERAL INFORMATION:
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92.9%;
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 92.9
Matches 13; Conservative
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Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-10-368-643-79
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US-10-138-316-79
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        APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Publication No. US20030054380A1
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Sanguinetti, Michael C.
APPLICANT: Splawski, Igor
IIILE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN minK WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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) OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.4; DB 22;
Pred. No. 1.9e+04;
0; Mismatches 1;
                                                                                FILE REFERENCE: 1179/1/US
CURRENT APPLICATION NUMBER: US/10/671,395
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 60/413,549
PRIOR FILING DATE: 2002-09-25
NUMBER OF SEQ ID NOS: 1809
SOFTWARE: PatentIn version 3.2
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ACTCTTGCAGGAAGCGGCT 20
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Best Local Similarity 92.9%;
Matches 13; Conservative
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62.0%;
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-911-678-79
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-861-520-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20
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                                                                                 Sequence 161, Application US/10714796
; Publication No. US20040180847A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Roller, Erich
; TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: ISTT-1004
; CURRENT APPLICATION NUMBER: US/10/714,796
; CURRENT PILING DATE: 2003-11-17
; PRIOR PILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 237
; SEQ ID NO 161
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 19;
Pred. No. 1.9e+04;
0; Mismatches 1;
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Pred. No. 1.9e+04;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TCTTGCAGGAAGCG 17
TGCAGGAAGCGGCT 20
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                         18 TGCAGGAAGCGGAT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             20 TCTTGCAGGAAGTG 7
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Mus musculus
US-10-714-796-161
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-10-714-796-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-714-796-161/C
                                                                               US-10-714-796-129/c
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Sequence 79, Application US/10911678

Publication No. US20050003439A1

GENERAL INPORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Splawski, Igor

ITIES OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING

TITLE OF INVENTION NUMBER: 09/144, 295

PRIOR FILING DATE: 1998-11-2

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 114

SSOFTWARE PATENTIN VOY: 2.0
TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH TITLE OF INVENTION: MUTATIONS IN THE KCNEI GENE ENCODING HUMAN mink WHICH TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING FILE REFERENCE: 2323-167

CURRENT APPLICATION NUMBER: US/10/861,520

CURRENT APPLICATION NUMBER: US/10/861,520

PRIOR PILING DATE: 2002-06-06

PRIOR PILING DATE: 2002-05-06

PRIOR PILING DATE: 1999-11-22

PRIOR PILING DATE: 1999-11-22

PRIOR PILING DATE: 1999-08-29

PRIOR PILING DATE: 1995-10-68

PRIOR PILING DATE: 1995-10-29

PRIOR PILING DATE: 1995-10-29

PRIOR PILING DATE: 1995-10-29

PRIOR PILING DATE: 1995-12-22

PRIOR PILING DATE: 1996-10-29

PRIOR PILING DATE: 1998-07-29

PRIOR PILING DATE: 1998-07-29
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Pred. No. 1.9e+04;
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Sequence Blit4, Application US/10723361
| Sequence Blit4, Application US/10723361
| Publication No. US2004017589A1
| Publication No. US2004017589A1
| Publication No. US2004017589A1
| APPLICANT: UI, Yonggang APPLICANT: UI, Yonggang APPLICANT: HAXZEL, David K. APPLICANT: HAXZEL, David K. APPLICANT: RANK, David K. APPLICANT: RANK, David K. APPLICANT: CHEN, Wensheng APPLICANT: CHEN, Wensheng APPLICANT: BANK, David K. APPLICANT: CHEN, Wensheng APPLICANT: BANK, DAVID MARK: US/10/723,361
| CURRENT APPLICANTON NUMBER: US/00/205.26
| PRIOR FILING DATE: 2001-05-25
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2000-01-30
| PRIOR FILING DATE: 2001-01-30
| PRIOR PRILOR DATE: 2001-01-30
                                     Sequence 544, Application US/09730289B

Sequence 544, Application No. US20030050259A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: MCSwiggen, Jim
TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease
TITLE OF INVENTION: WHENE: US/09/730,289B
CURRENT FILING DATE: 2000-12-05
PRIOR PPLICATION NUMBER: US 60/169,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3897
SOFTWARE: PatentIn version 3.0
SEQ ID NO 544
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SOFTWARE: Aeomica Sequence Listing Engine
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Best Local Similarity 82.4<sup>†</sup>
Matches 14<sup>‡</sup>, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
ORGANISM: Homo sapiens
US-09-730-289B-544
                          IS-09-730-289B-544/C
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APPLICANT: CHEN, Wencheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                  Score 12.4; DB 21; Length 20; Pred. No. 1.9e+04; 0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE KEKERKENE: ALCHICA-CA-CURRENT PERLENGENCE: ALCHICA-CA-CURRENT PELLING DATE: 2001-05-25
PRIOR PELLING DATE: 2001-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-07
PRIOR PELLING DATE: 2000-10-27
PRIOR PELLING DATE: 2000-10-27
PRIOR PELLING DATE: 2001-01-30
P
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8114, Application US/09866108
Patent No. US20020048800A1
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                                 62.0%;
92.9%;
                                                                                                                                                                                 7 TGCAGGAAGCGGCT 20
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HANZEL, David K.
Query Match
Best Local Similarity 92.5-
Local 31 Conservative
                                                                                                                                                                                                                                                        18 TGCAGGAAGCGGAT 5
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CORGANISM: Homo sapiens
US-09-866-108-8114
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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumenkov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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US-10-719-956-271624/C
US-10-719-956-271624, Application US/10719956

Sequence 271624, Application US/10719956

Publication No. US20040146910A1

GREERAL INFORMATION:

APPLICANT: Xue and Zhou

TITLE OF INVENTION:

FILE REFERENCE: 3527.1

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,836

FRIOR APPLICATION UNBER: 60/427,836

NUMBER OF SEQ ID NOS: 699466

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 271624

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                         APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900.
CURRENT PILING DATE: 2003-11-20
PRIOR PILING DATE: 2002-11-20
NUMBER: OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 383106
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.0%; Score 12.2; DB 21;
Best Local Similarity 82.4%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 3;
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Pred. No. 2.4e+04;
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                                                                                                                                                              ; Sequence 383106, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8500, Application US/10349143 Publication No. US20040005584A1 GENERAL INFORMATION:
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4 TCTTGCAGGAAGCGGCT 20
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Best Local Similarity 82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Rattus norvegicus US-10-719-956-271624
                                              19 rccrecaccaagreerr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-10-719-900-383106
                                                                                                                        RESULT 35
US-10-719-900-383106/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                          Sequence 507, Application US/10671395

Sequence 507, Application US/10671395

Publication No. US20040132063A1

GENERAL INFORMATION:
APPLICANT: Paramacia Corp.
APPLICANT: Gierse, James K
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: ANTISENSE NODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE
TITLE OF INVENTION: BAPRICATION NUMBER: US/10/671,395
CURRENT APPLICATION NUMBER: G0/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
PRIOR APPLICATION NUMBER: 60/413,549
SROFTWARE: Parent In version 3.2

SEQ ID NO 507

LENGTH: 20
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; Sequence 692, Application US/10671395
; Publication No. US20040132063A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.;
; APPLICANT: Glarge, James K
; TITLE OF INVENTION: ANTISENSE MODULATION OF MICROSOMAL PROSTAGLANDIN E2 SYNTHASE;
; TITLE OF INVENTION: ANTISENSE NOUNBER: US/10/671,395
; TITLE REFRENCE: 1179/1/US
; CURRENT APPLICATION NUMBER: US/10/671,395
; CURRENT FILING DATE: 2002-09-25
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 1809
; SOFTWARE: Patentin version 3.2
; LENGTH: 20
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                                                                          Length 17;
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                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                     Query Match 61.0%; Score 12.2; DB 19;
Best Local Similarity 82.4%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.0%; Score 12.2; DB 19;
Best Local Similarity 82.4%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 3;
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Best Local Similarity 82.4%; Pred. No. 2.4e+04;
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; OTHER INFORMATION: Human PGE2 antisense
US-10-671-395-692
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; OTHER INFORMATION: Human PGE2 antisense US-10-671-395-507
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; ORGANISM: Homo sapiens
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Sequence 997, Application US/09780533A
; Sequence 997, Application No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Growitz, Blatt, Larry
; APPLICANT: Growitz, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; TITLE OF INVENTION: Method, 278-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; MUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 997
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    TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
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Pred. No. 3.8e+04;
0; Mismatches 2;
                       FILE REFERENCE: MBHB00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: US 60/181,797
FRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: Patentin version 3.0
SEQ ID NO 92
LENGTH: 17
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86.7%;
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Best Local Similarity 86.75
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 13; Conserv
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) LOCATION: 1..20

) OTHER INFORMATION: downstream amplification primer 99-15968 for SEQ 635, in compleme

US-10-349-143-8500
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Sequence 91, Application US/09780533A

Publication No. US2030060611A1

SEQUENCE INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Blatt, Larry

APPLICANT: Blatt, Larry

APPLICANT: Habbril, Pete

TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene

FILE REFERENCE: MBHB00, 878-A (400/011)

CURRENT APPLICATION NUMBER: US/09/780,533A

CURRENT APPLICATION NUMBER: US 60/181,797

PRIOR FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR PELING DATE: 1999-10-20

PRIOR PELING DATE: 1999-10-20

PRIOR PILING DATE: EARLIER PILING DATE: 1999-04-21

PRIOR PILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

LENGTH: 20
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Best Local Similarity 75.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 5; Indels
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SOFWARE: Patentin version 3.0
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Best Local Similarity 86.7
Matches 13; Conservative
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US-09-780-533A-91
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AZ816318 2M00055H05
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AZ631554

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AUTHORS
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1M0031G07F Mouse 10kb plasmid
clone UUGC1M0031G07 F, genomic
AZ314365
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Seq primer: CGTIGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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University of Utah Genome Center
University of Utah
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AZ314365.1 GI:10360181
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Fax: 801 585 7177
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1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B.,
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            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="UUGC1M0031G07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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Query Match

53.0%;

Score 10.6;

DB

8

Length 20

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RESULT 2
AJ650912/c
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ORGANISM
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CD532073/c
LOCUS
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ORGANISM
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    AUTHORS
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Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Sitel: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
Location/Qualifiers
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AJ650912
                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, S.I., Finlayson, H.A. and Archibald, A.L. Development of cDNA and EST resources for studying embryo development in pigs and cattle
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Sus scrofa
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EST.
                                                                                                                                                                          3', mRNA sequence.
CD532073
                                                                                                                                                                                                                                      CD532073
                                                                                                                Arabidopsis thaliana (thale cress)
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Roslin, Midlothian,
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o,Y., Cai,Z. and
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mol type="mRNA"
/db_xref="taxon:9823"
/clone="C0003276_L01"
/tissue type="ovary"
/clone_lib="CSEQRAN19"
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NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"
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    and Gan, S
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Pred. No. 2e+06;
D; Mismatches 1;
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cofa cDNA clone C0003276_L01,
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Sus.
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                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0497 row: D column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornell University
119 Plant Science,
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Department of Horticulture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ637794 20 bp DNA linear GSS 13-DEC-200 1M0497D20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0497D20 F, genomic survey sequence.
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Insert Length: 19 Std Error: 0.00
                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Mus musculus (house mouse)
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AZ637794.1 GI:11759984
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quality sequence stop: 20 
Location/Qualifiers
                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Leaf"
/dev_stage="Yellow Leaf With Greenish Base Area"
/lab_host="E._coli"
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/mol_type="mRNA"
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Pred. No. 2.6e
0; Mismatches
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: J column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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20 bp DNA linear GSS 29-SEP-200
1M0066J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0066J13 R, genomic survey sequence.
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/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 2.6e+06;
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                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: L column: 02
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ410317 19 bp DNA linear GSS 03-OCT-2011M0182L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC1M0182L02 R, genomic survey sequence.
                                                                                                                                                                         Tel: 801 585 5606 Fax: 801 585 7177
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quality sequence stop: 19.
Location/Qualifiers
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/strain="C57BL/6J"
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                       Seq primer: CGTTGTAAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 19.
                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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University of Utah
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/strain="C57BL/6J"
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Pred. No. 6.3e+06;
D; Mismatches 1; Indels
                                                                                                                              Std Error: 0.00
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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0055 row: H column: 05
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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Nouse whole genome scaffolding with paired end reads from 10kb
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University of Utah
Rm. 308, Biomedical
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
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/mol_type="genomic DNA"
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Pred. No. 6.3e+06;
0; Mismatches 1;
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     Email: ddunn@genetics.utah.edu
Insert i.ength: 10000 Std Error: 0.4
Plate: 0307 row: L column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Unpublished (2000)
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19 bp DNA linear GSS 05-OCT-201
1M0307L16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0307L16 R, genomic survey sequence.
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                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0055H05"
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Pred. No. 6.4e+06;
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                                                                                                                                                          Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                           Max-Planck-Institute for Developmental Spemannstr. 37-39, Tuebingen D-72076, GTel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                             Pristionchus pacificus
Nucleic Acids Res. 32 (1),
Contact: Sommer RJ
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Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                            Evolutionary Biology
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Neodiplogasteridae; Pristionchus.
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
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/strain="C57BL/6J"
                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                             l Biology
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                                                                                                                                                                                                                                                                                                                                          source
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Contact: Hall N
Pathogen Sequencing Unit
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
The Sanger Institute The Wellcome Trust Genome Campus
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ω
                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                         School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting
end of the cDNA all pic reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BX559186 Glossina morsitans morsitans adult infected gut Gl morsitans morsitans cDNA clone Tse42b02_q1c, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response genes
Genome Biol. 4 (10), R63 (2003)
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                                   CTCTTGCAGGAAGCGGC 19
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CTCTAGTAAGAAGTGAC 19
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                                                                                                                                                                                                          /clone="Tse42b02 glc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                             /note="country: Zimbabwe;
r.brucei"
                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/sub_species="morsitans"
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                                                                                                                                                                                                                                                                                                                       organism="Glossina morsitans morsitans"
                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                       xref="taxon:37546"
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1e+07;
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RESULT 12

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ORGANISM
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BQ587767.1
EST.
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1 (bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ587767 16 bp mRNA linear EST 06-DEC E012340w-024-010-M01-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-010-M01 5-PRIME, mRNA sequence.
                                   1M0302N15R Mouse 10kb plasmid UUGC1M library Muclone UUGC1M0302N15 R, genomic survey sequence. AZ481008 GI:10641989 GSS.
                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 10 row: M column: 01
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta vulgaris
                                                                                                                                       AZ481008
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musculus
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                  musculus (house mouse)
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="MPIZ-ADIS-024-Lear"
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saarzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                     RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SP6-Sall-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GABI:185096"
/db_xref="taxon:161934"
/clone="024-010-M01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tom/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
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tivar="KWS2320 (double haploid, monogerm breeding
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                                                                                                                                                                                                                                                                                                                 Score 8.8; DB 5; Length 16;
Pred. No. 1.2e+07;
0; Mismatches 2; Indels
                                                                                                                    19 bp DNA linea:
mid UUGC1M library Mus
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                                                                                                                    musculus genomic
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                                                                                                               AZ959942
2M0227L13R Mouse 10kb plasmid
clone UUGC2M0227L13 R, genomic
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High quality sequence stop: 19.
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Plate: 0302 row: N column:
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Insert Length: 10000 Std Error: 0.00
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B. Weiss
University of Utah
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC
                                                                           AZ959942.1
                                                                                                    AZ959942
                                                                                                                                                                                                                                                                                                      CAGAAAGCAGCT 7
                                                                                                                                                                                                                                                                                                                                             CAGGAAGCGGCT 20
musculus
                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored work passage and annealed to adaptored work passage and paraferral vector NNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
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                                                                           GI:13831169
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                       (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 8.8; DB 8;
Pred. No. 1.2e+07;
0; Mismatches 2
                                                                                                                         genomic survey sequence
                                                                                                                                                bp DNA linear GSS 27-APK-20
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Insert Length: 10000 Std Error: 0.00
Plate: 0227 row: L column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Welss,R.
AJ599745
AJ599745.1 GI:37949373
GSS; left border; T-DNA flanking sequence
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 19)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                  AJ599745 20 bp DNA li
Arabidopsis thaliana T-DNA flanking sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_bost="E. coli strain XL10-Gold, T1-resistant,
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
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/clone="UUGC2M0227L13"
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/strain="C57BL/6J"
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Best Local Similarity
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Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/ This sequence has been generated in the framework of the French plant genomics been Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                               AJ587896. GI:37937520
AJ587895.1 GI:37937520
GSS; left border; T-NA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 bp 1
Arabidopsis thaliana T-DNA flanking
337H10, genomic survey sequence.
AJ587896
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Direct Submission
                                                                                          Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F. Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
                                                             I-DNA integration into the Arabidopsis
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pre-insertion sites
30 Rep. 3 (12), 1152-1157 (2002)
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left border"
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/clone="492G09"
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'cultivar="Wassillewskija"
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Pred. No. 1.6e+07;
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                                                                    genome depends on sequences
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RESULT 17
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AZ397615.1 GI:10512687
GSS.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 19)
1 (Dases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0162 row: M column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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Unpublished (2000)
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                                                                                                          High quality sequence stop: 19
                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center
University of Utah
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1. .16
/organism="Mus musculus"
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left border"
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/mol_type="genomic DNA"
/cultiva="Wassillewskija"
/db_xref="taxon:3702"
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Pred. No. 1.9e+07;
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Query Match
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19 bp DNA linear GSS 03-OCT-200
1M0197I07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0197I07 R, genomic survey sequence.
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                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0197 row: I column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
                                                           Location/Qualifiers
/organism="Mus musculus"
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Pred. No. 2e+07;
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                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: I column: 23
Seq primer: CGTTCTAAAACGACGGCCAGT
Class: plasmid ends
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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1M0552I23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                              Location/Qualifiers
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/strain="C57BL/6J"
organism="Mus musculus"
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'clone="UUGC1M0197I07"
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Pred. No. 2e+07;
0; Mismatches
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University of Utah Genome Center
University of Utah
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Matches Query Match ORIGIN

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the innert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0552123"
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DB 8; Length 19;
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Similarity 9; Conserv Conservative 42.0%; Score 8.4; DB 8 Pred. No. 2e+07; 0; Mismatches 1,

0

Gaps

0

AZ597307 20 bp DNA linear GSS 13-DEC-20-1M0410N24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0410N24 R, genomic survey sequence. GSS 13-DEC-2000

Mus musculus Mus musculus (house mouse) AZ597307.1 GI:11719413

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION AZ759607 RESULT 19

REFERENCE

AUTHORS

COMMENT

JOURNAL TITLE

FEATURES

source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

plasmid inserts Unpublished (2000) Mouse whole genome scaffolding with paired end reads from 10kb

Tel: 801 585 5606 Fax: 801 585 7177 308, USA Biomedical Polymers Research Bldg., 20 S. 2030 ; SLC,

S

Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: (Plate: 0410 row: N column: 24 Seq primer: CACACAGGAAACAGCTATGACC High quality sequence stop: 20 Class: plasmid ends Location/Qualifiers Std Error: 0.00

/organism="Mus musculus"

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RESULT 21
AZ827842
LOCUS
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AZ827842
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GSS.
                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: F column: 03
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                  University of Utah (University of Utah Rm. 308, Biomedical
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                                                                                        Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                                            quality sequence stop: 20.
Location/Qualifiers
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801 585 7177
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/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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/clone="UUGC1M0410N24"
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/strain="C57BL/6J"
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/organism="Mus musculus"
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SOURCE

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KEYWORDS

FEATURES

Vector : pBACe3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI. Location/Qualifiers

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: RP43-063J03.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J., Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
                                                                                                                                        of clone tracking errors.
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                                   Sequencing: T7
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/strain="C57BL/6J"
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Pred. No. 2e+07;
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sapiens cDNA

EST 30-JUN-1998

Project (CGAP),

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RESULT 23
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RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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BQ789829.1 GI:22004791
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9; Conservative
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Pinus sylvestris/Heterobasidion annosum mixed EST library
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/sex="male"
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/dev_stage="Seedling roots of scots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:169015"
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/clone_lib="RP-43 Chimpanzee Male BAC Library"
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Pred. No. 2
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Pred. No. 2.3e+07;
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C00629
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality
Seq.primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI042533 18 bp mRNA linear oy06e03.x1 Soares senescent fibroblasts NbHSF Homo clone IMAGE:1665052 3' similar to TR:Q15662 Q15662 TRANSFORMATION-RELATED PROTEIN ;, mRNA sequence.
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                                                                        BodyMap; human gene
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                              C00629 18 bp
HUMGS0008172 Human adult (K.Okubo)
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
                             Contact: Okubo, K.
Institute for Molecular
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18)
                                                                                                                                                                                                                                     Homo sapiens
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     Osaka University
                                                                                                                              Okubo, K.
                                                                                                                                                                                                                                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="senescent fibroblast"
/lab host="DH108 (ampicillin resistant)"
/clone lib="Soares senescent fibroblasts NbHSF"
/clone Lib="Soares senescent fibroblasts NbHSF"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st_strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:1665052"
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76.9%;
                                                                                                      expression database
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Pred. No. 2.4e+07;
                             and Cellular Biol
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Homo sapiens cDNA, mRNA
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Indels

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EST 31-DEC-2002

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JOURNAL COMMENT
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AUTHORS
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CL661466
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Matches 10
                                                    Query Match
Best Local Similarity
                                      Matches
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                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                       Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CL661466
CL661466.1 GI:50147979
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CL661466 18 bp DNA PRIO139d_GO2 - PRIO139d_B21 (18) Mixed pacificus var. California Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1993. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see' http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-3, Yamada-oka, Suita,
Tel: 06-877-5111 (ex.331
Email: kousaku@imcb.osa
                                                                                                                                                                                                                                                                                                                                                                                                      Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa; Nematoda, Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 GACTCTTGCAGGA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolutionary Biology
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                                                                                                                                                   /db_xref="taxon:54126"
/clone_lib="Mixed stage
var. California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="One or more human
                                                                                                                                                                                                            organism="Pristionchus pacificus"
| mol_type="genomic DNA"
| strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                   /note="Vector: pEpifos-5
                                                                                                                                                                                                                                                                                       location/Qualifiers
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                                                      41.0%;
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"One or more human adult tissue"
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Pred.
                                    Score 8.2; DB 9;
Pred. No. 2.4e+07;
D; Mismatches 3;
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No. 2.4e+07;
                                                                                                                                                                          fosmid library of P.
                                                                                                                                     Fosmid vector"
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AJ666428
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AJ666428
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                                                                                                                                                                                                                                BQ587387 19 bp mRNA

$014305-024-010-H05-SP6 MPIZ-ADIS-024-leaf

024-010-H05 5-PRIME, mRNA sequence.

BQ587387

BQ587387.1 GI:26116969
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Roslin, Vectoring BlueScriptII (KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 19)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying
embryo development in pigs and cattle
Unpublished (2004)
                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 19)
                                                                                                                                                                        Beta vulgaris
Beta vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (pig)
Sus scrofa
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Construction of a 'unigene' cDNA clone fingerprinting allows access to 25 000
                                          and Radelof, U.
                                                          Drungowski,M., Stahl,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/mol type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_N10"
/tissue_type="placenta"
/clone_Tib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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                                                          Weisshaar,B., Hennig,S., Steinfath,M.,
D., Wruck,W., Menze,A., O'Brien,J., Leb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8.2; DB 1;
Pred. No. 2.4e+07;
); Mismatches 3
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    set by oligonucleotide . potential sugar beet genes
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Sus.
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                                                                  Lehrach, H.
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845-857 (2002)

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22362189
12472698
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1M0109P06R Mouse 10kb plasmid
clone UUGC1M0109P06 R, genomic
AZ363824
AZ363824.1 GI:10477524
GSS.
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                                                                                                                                    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: weisshaa@mpiz-koeln.mpg.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                    plasmid inserts
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ddunn@genetics.utah.edu
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/lab_host="EMDH10B"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
/note="MPIZ-ADIS-024-leaf"
/tissue_type="leaf"
/clone="MPIZ-ADIS-024-leaf"
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Nouse whole genome scaffolding with paired end reads from 10kb
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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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Plate: 0109 row: P column: 06
Seq primer: CACACAGAAACAGCTATGACC
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                                                                                                                                                                              plasmid inserts
Unpublished (2000)
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AZ422762.1
                                                                                    University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                             Contact: Robert B.
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                                                                   USA
ddunn@genetics.utah.edu
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42ny; Purified genomic DNA from I
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  84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Seq primer: CACACAGGAAACAGCTATGACC
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19 bp DNA linear GSS 05-OCT-201
1M0351A21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0351A21 R, genomic survey sequence.
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                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
                                                                                                                                                                                                                                                             Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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AZ509071.1 GI:10690387
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ddunn@genetics.utah.edu
                                                                                               Biomedical Polymers Research Bldg.,
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
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/clone="UUGC1M0201P12"
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/strain="C57BL/6J"
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AZ626779
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Plate: 0351 row: A column: 21
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ626779 19 bp DNA linear IM0467A14F Mouse 10kb plasmid UUGCIM library Mus clone UUGCIM0467A14 F, genomic survey sequence.
AZ626779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                     1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                           University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                           Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                        Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                   plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ626779.1
Email: ddunn@genetics.utah.edu
                                                                                                                                                                     Contact: Robert
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308,
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/ (lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/ (clone lib="Mouse 10kb plasmid UUGCIM library"
/ (clone lib="Mouse 10kb plasmid UUGCIM library"
/ (note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|473114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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76.9%;
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RESULT 33
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                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 20)
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Unpublished (2000)
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AZ410583.1 GI:10534512
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1M0182E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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/strain="C57BL/6J"
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/clone="UUGC1M0467A14"
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76.9%;
                                                                                             Polymers Research
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T. brucei sheared genomic genomic survey sequence.
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( to give a tight size distribution ( 4\ \rm kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In
                                                                                                                                                                                                                         Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, B-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 20)
Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
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AL475823.1 GI:11842591
                                                                                                                                                                                                     nh1@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="C57BL/6J"
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Pred. No. 2.5e+07;
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Insert Length: 444 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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similar to SW:BI3_MOUSE
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH108"
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/clone libs "NCI_CGAP_LUS; Vector: pT7T3D-Pac (Pharmacia) with a /note="Double-stranded cond with a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was pT7T3 vector by Bento Soares and M. Fatima Bonaldo. "
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="207b03"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1556632"
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VERSION
KEYWORDS
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CNS09MAX/c
                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
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AZ500630
LOCUS
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS09MAX 19 bp mRNA linear HTC 08-JAN-20 Single read from an extremity off a full-length cDNA clone made fi Anopheles gambiae total adult females. 3-PRIME end of clone FKOAAC48CF12 of strain 6-9 of Anopheles gambiae (African malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                               AZ500630 19 bp DNA linear 1M0339A10F Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0339A10 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryo
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX064981.1
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Unpublished (2000)
Contact: Robert B.
University of Utah
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                                                                                                                                                                                                    Mus musculus
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                                                                   Mouse whole genome scaffolding with
                                                     plasmid
                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                     AZ500630.1 GI:10680639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                     inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7165"
/clone="FKOAAC48CF12"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="6-9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:27638262
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Pred. No. 3.1e
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Matches
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Best Local (
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AZ814554.1
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Insert Length: 10000 Std Error:
Plate: 0339 row: A column: 10
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                19 bp DNA linear GSS 20-FEB-20
2M0082P13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0082P13 F, genomic survey sequence
AZ814554
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Location/Qualifiers
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Fax: 801 585 7177
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Rm. 308, Biomedical
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                                                                      plasmid inserts
                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
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/strain="C57BL/6J"
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Pred. No. 3.1
0; Mismatches
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3.1e+07;

ches 0; Indels
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RESULT 39
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ORGANISM
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Best Local
                                                                                                                                                 AUTHORS
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                                                                   1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., L.
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                         20 pp mRNA linear EST 15-AUG-2003 HDA1--01-C09.gl OsHDAC1-overexpressing transgenic rice lambda phage cDNA library I (HDA1) Oryza sativa (japonica cultivar-group) cDNA clone HDA1--01-C09, mRNA sequence. CF305590
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Insert Length: 10000 Std Error:
Pollum: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel elettrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="genomic
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="UUGC2M0082P13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:10090"
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                                                                                                                                                 Shin, Y.C.,
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JOURNAL COMMENT
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AUTHORS
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ORGANISM
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. V
University of Utah (
University of Utah
                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: N column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse, whole genome scaffolding with paired end reads from 10kb Notes, whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ366451 20 bp DNA linear GSS 02-OCT-200 1M0115N07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0115N07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 TGCAGGAA 14
                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Mus musculus
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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8; Conserv
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usa
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="HDA1--01-C09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E_coli SOLR"
                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0115N07"
                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.0%; Score 8; DB 7
100.0%; Pred. No. 3.1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Genome Center
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                                                                                                                                                                                                                                                                                                                                                         20 S. 2030 E.,
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWN2 (gi|4732114|gb|AF129072-1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Matches 8; Conservative 0; Mismatches

10 AGGAAGCG 17

|||||||
6 AGGAAGCG 13

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ORIGIN

Query Match Best Local S

Similarity

40.0%; Score 8; DB 8; Length 20; 100.0%; Pred. No. 3.1e+07;

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Search completed: August 6, 2005, 16:28:28 Job time: 1629 secs

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